

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: BROW, MARY ANN D.  
LYAMICHEV, VICTOR I.  
OLIVE, DAVID M.

(ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
PATHOGENS

(iii) NUMBER OF SEQUENCES: 160

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MEDLEN & CARROLL  
(B) STREET: 220 MONTGOMERY STREET, SUITE 2200  
(C) CITY: SAN FRANCISCO  
(D) STATE: CALIFORNIA  
(E) COUNTRY: UNITED STATES OF AMERICA  
(F) ZIP: 94104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Patentin Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CARROLL, PETER G.  
(B) REGISTRATION NUMBER: 32,837  
(C) REFERENCE/DOCKET NUMBER: FORS-01756

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2506 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|  |     |
|--|-----|
| ATGAGGGGGA TGCTGCCCTT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC  | 60  |
| CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCTCA CCACCAGCCG GGGGGAGCCG   | 120 |
| GTGCAGGCAGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC | 180 |
| GCGGTGATCG TGGTCTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG   | 240 |
| TACAAGGCAGG GCCGGGCCCG CACGCCGGAG GACTTTCCCC GGCAACTCGC CCTCATCAAG | 300 |

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|             |            |             |            |             |             |      |
|-------------|------------|-------------|------------|-------------|-------------|------|
| GAGCTGGTGG  | ACCTCCTGGG | GCTGGCGCGC  | CTCGAGGTCC | CGGGCTACGA  | GGCGGACGAC  | 360  |
| GTCCTGGCCA  | GCCTGGCAA  | GAAGGCGGAA  | AAGGAGGGCT | ACGAGGTCCG  | CATCCTCACCC | 420  |
| GCCGACAAAG  | ACCTTTACCA | GCTCCTTCC   | GACCGCATCC | ACGTCTCCA   | CCCCGAGGGG  | 480  |
| TACCTCATCA  | CCCCGGCCTG | GCTTTGGGAA  | AAGTACGGCC | TGAGGCCCGA  | CCAGTGGGCC  | 540  |
| GAATACCGGG  | CCCTGACCGG | GGACGAGTCC  | GACAACCTTC | CCGGGGTCAA  | GGGCATCGGG  | 600  |
| GAGAAGACGG  | CGAGGAAGCT | TCTGGAGGAG  | TGGGGGAGCC | TGGAAGCCCT  | CCTCAAGAAC  | 660  |
| CTGGACCGGC  | TGAAGCCCAG | CATCCGGGAG  | AAGATCCTGG | CCCACATGGA  | CGATCTGAAG  | 720  |
| CTCTCCTGGG  | ACCTGGCAA  | GGTGCGCACC  | GACCTGCC   | TGGAGGTGGA  | CTTCGCCAAA  | 780  |
| AGGCGGGAGC  | CCGACCGGGA | GAGGCTTAGG  | GCCTTCTGG  | AGAGGCTTGA  | TTTGGCAGC   | 840  |
| CTCCTCCACG  | AGTTCGGCCT | TCTGGAAAGC  | CCCAAGGCC  | TGGAGGAGGC  | CCCCTGGCCC  | 900  |
| CCGCCGGAAG  | GGGCCTTCGT | GGGCTTTGTG  | CTTCCCAGCA | AGGAGCCAT   | GTGGGCCGAT  | 960  |
| CTTCTGGCCC  | TGGCCGCCGC | CAGGGGGGGC  | CGGGTCCACC | GGGCCCCCGA  | GCCTTATAAA  | 1020 |
| GCCCTCAGGG  | ACCTGAAGGA | GGCGCGGGGG  | CTTCTCGCCA | AAGACCTGAG  | CGTTCTGGCC  | 1080 |
| CTGAGGGAAG  | GCCTTGGCCT | CCCGCCCGGC  | GACGACCCCA | TGCTCCTCGC  | CTACCTCCTG  | 1140 |
| GACCCTTCCA  | ACACCACCCC | CGAGGGGGTG  | GCCCGCGCT  | ACGGCGGGGA  | GTGGACGGAG  | 1200 |
| GAGGCGGGGG  | AGCGGGCCGC | CCTTTCCGAG  | AGGCTTTCTG | CCAACCTGTG  | GGGGAGGCTT  | 1260 |
| GAGGGGGAGG  | AGAGGCTCCT | TTGGCTTTAC  | CGGGAGGTGG | AGAGGCCCCT  | TTCCGCTGTC  | 1320 |
| CTGGCCCACA  | TGGAGGCCAC | GGGGGTGCGC  | CTGGACGTGG | CCTATCTCAG  | GGCCTTGTCE  | 1380 |
| CTGGAGGTGG  | CCGAGGAGAT | CGCCCGCCTC  | GAGGCCGAGG | TCTTCCGCCT  | GGCCGGCCAC  | 1440 |
| CCCTTCAACC  | TCAACTCCCG | GGACCAGCTG  | GAAAGGTCC  | TCTTGACGA   | GCTAGGGCTT  | 1500 |
| CCCGCCATCG  | GCAAGACGGA | GAAGACCGGC  | AAGCGCTCCA | CCAGCGCCGC  | CGTCCTGGAG  | 1560 |
| GCCCTCCCGC  | AGGCCACCCC | CATCGTGGAG  | AAGATCCTGC | AGTACCGGGA  | GTCACCAAG   | 1620 |
| CTGAAGAGCA  | CCTACATTGA | CCCCTTGCG   | GACCTCATCC | ACCCCAGGAC  | GGGCCGCCTC  | 1680 |
| CACACCCGCT  | TCAACCAGAC | GGCCACGGCC  | ACGGGCAGGC | TAAGTAGCTC  | CGATCCCAAC  | 1740 |
| CTCCAGAACCA | TCCCCGTCCG | CACCCCGCTT  | GGGCAGAGGA | TCCGCCGGGC  | CTTCATCGCC  | 1800 |
| GAGGAGGGGT  | GGCTATTGGT | GGCCCTGGAC  | TATAGCCAGA | TAGAGCTCAG  | GGTGTGGGCC  | 1860 |
| CACCTCTCCG  | GCGACGAGAA | CCTGATCCGG  | GTCTTCCAGG | AGGGGCGGGGA | CATCCACACG  | 1920 |
| GAGACCGCCA  | GCTGGATGTT | CGGCGTCCCC  | CGGGAGGCCG | TGGACCCCT   | GATGCCGCCGG | 1980 |
| GCGGCCAAGA  | CCATCAACTT | CGGGGTCCCTC | TACGGCATGT | CGGCCACCG   | CCTCTCCCAG  | 2040 |
| GAGCTAGCCA  | TCCCTTACGA | GGAGGCCAG   | GCCTTCATTG | AGCGCTACTT  | TCAGAGCTTC  | 2100 |
| CCCAAGGTGC  | GGGCCTGGAT | TGAGAAGACC  | CTGGAGGAGG | GCAGGAGGCG  | GGGGTACGTG  | 2160 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| GAGACCCTCT | TCGGCCGCCG | CCGCTACGTG | CCAGACCTAG | AGGCCGGGT  | GAAGAGCGTG | 2220 |
| CGGGAGGCAG | CCGAGCCAT  | GGCCTTCAAC | ATGCCCGTCC | AGGGCACCGC | CGCCGACCTC | 2280 |
| ATGAAGCTGG | CTATGGTGAA | GCTCTTCCCC | AGGCTGGAGG | AAATGGGGGC | CAGGATGCTC | 2340 |
| CTTCAGGTCC | ACGACGAGCT | GGTCCTCGAG | GCCCCAAAAG | AGAGGGCGGA | GGCCGTGGCC | 2400 |
| CGGCTGGCCA | AGGAGGTCAT | GGAGGGGTG  | TATCCCCTGG | CCGTGCCCT  | GGAGGTGGAG | 2460 |
| GTGGGGATAG | GGGAGGACTG | GCTCTCCGCC | AAGGAGTGAT | ACCACC     |            | 2506 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2496 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|            |            |             |            |             |            |      |
|------------|------------|-------------|------------|-------------|------------|------|
| ATGGCGATGC | TTCCCTCTT  | TGAGCCAAA   | GGCCCGTGC  | TCCTGGTGA   | CGGCCACCAC | 60   |
| CTGGCCTACC | GCACCTCTT  | TGCCCTCAAG  | GGCCTCACCA | CCAGCCGCGG  | CGAACCCGTT | 120  |
| CAGGCGGTCT | ACGGCTCGC  | CAAAGCCTC   | CTCAAGGCC  | TGAAGGAGGA  | CGGGGACGTG | 180  |
| GTGGTGGTGG | TCTTGACGC  | CAAGGCCCCC  | TCCTTCCGCC | ACGAGGCCTA  | CGAGGCCTAC | 240  |
| AAGGCGGGCC | GGGCCCCCAC | CCCGGAGGAC  | TTTCCCCGGC | AGCTGGCCCT  | CATCAAGGAG | 300  |
| TTGGTGGACC | TCCTAGGCCT | TGTGCGGCTG  | GAGGTTCCCG | GCTTTGAGGC  | GGACGACGTG | 360  |
| CTGGCCACCC | TGGCCAAGCG | GGCGGAAAAG  | GAGGGTACG  | AGGTGCGCAT  | CCTCACTGCC | 420  |
| GACCGCGACC | TCTACCAGCT | CCTTTCGGAG  | CGCATCGCCA | TCCTCCACCC  | TGAGGGTAC  | 480  |
| CTGATCACCC | CGGCGTGGCT | TTACGAGAAG  | TACGGCCTGC | GCCCCGGAGCA | GTGGGTGGAC | 540  |
| TACCGGGCCC | TGGCGGGGGA | CCCCTCGGAT  | AACATCCCCG | GGGTGAAGGG  | CATCGGGGAG | 600  |
| AAGACCGCCC | AGAGGCTCAT | CCCGCGAGTGG | GGGAGCCTGG | AAAACCTCTT  | CCAGCACCTG | 660  |
| GACCAGGTGA | AGCCCTCCTT | GCGGGAGAAG  | CTCCAGGCCG | GCATGGAGGC  | CCTGGCCCTT | 720  |
| TCCCGGAAGC | TTTCCCAGGT | GCACACTGAC  | CTGCCCTGG  | AGGTGGACTT  | CGGGAGGCGC | 780  |
| CGCACACCCA | ACCTGGAGGG | TCTGCGGGCT  | TTTTTGGAGC | GGTTGGAGTT  | TGGAAGCCTC | 840  |
| CTCCACGAGT | TCGGCCTCCT | GGAGGGGCCG  | AAGGCGGCAG | AGGAGGCC    | CTGGCCCCCT | 900  |
| CCGGAAGGGG | CTTTTTGGG  | CTTTTCCTTT  | TCCCGTCCCG | AGCCCATGTG  | GGCCGAGCTT | 960  |
| CTGGCCCTGG | CTGGGGCGTG | GGAGGGGCCG  | CTCCATCGGG | CACAAGACCC  | CCTTAGGGC  | 1020 |
| CTGAGGGACC | TTAAGGGGT  | GCGGGGAATC  | CTGGCCAAGG | ACCTGGCGGT  | TTTGGCCCTG | 1080 |
| CGGGAGGGCC | TGGACCTCTT | CCCAGAGGAC  | GACCCATGC  | TCCTGGCCTA  | CCTTCTGGAC | 1140 |

CCCTCCAACA CCACCCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT 1200  
 GCAGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCAGA CCCTAAAGGA GCGCCTTAAG 1260  
 GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGAGA AGCCGCTTTC CGGGGTGTTG 1320  
 GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG 1380  
 GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC 1440  
 TTCAACCTCA ACTCCCGCGA CCAGCTGGAG CGGGTGCCTCT TTGACGAGCT GGGCCTGCCT 1500  
 GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC 1560  
 CTGCGAGAGG CCCACCCAT CGTGGACCAC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC 1620  
 AAGAACACCT ACATAGACCC CCTGCCCGCC CTGGTCCACC CCAAGACCGG CGGGCTCCAC 1680  
 ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCAACCTG 1740  
 CAGAACATCC CCGTGCAC CGCCCTGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG 1800  
 GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCCAC 1860  
 CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTCAGGAGG GGAGGGACAT CCACACCCAG 1920  
 ACCGCCAGCT GGATGTCGG CGTTTCCCCC GAAGGGTAG ACCCTCTGAT GCGCCGGCG 1980  
 GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCAATGTCCG CCCACCGCCT CTCCGGGAG 2040  
 CTTTCCATCC CCTACGAGGA GGCAGGCTGC TTCATTGAGC GCTACTTCCA GAGCTACCCC 2100  
 AAGGTGCGGG CCTGGATTGA GGGGACCCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG 2160  
 ACCCTCTTCG GCCGCCGGCG CTATGTGCC GACCTAACG CCCGGGTGAA GAGCGTGCAC 2220  
 GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG 2280  
 AAGCTGGCCA TGGTGCCTGCT TTTCAGGAAAC TGGGGGCGAG GATGCTTTG 2340  
 CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCCAAGGACC GGGCGGAGAG GGTAGCCGCT 2400  
 TTGGCCAAGG AGGTCACTGGA GGGGGTCTGG CCCCTGCAGG TGCCCCCTGGA GGTGGAGGTG 2460  
 GGCTGGGGG AGGACTGGCT CTCCGCCAAG GAGTAG 2496

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2504 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|   |     |
|---|-----|
| ATGGAGGCGA TGCTTCCGCT CTTTGAACCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC | 60  |
| CACCTGGCCT ACCGCACCTT CTTCGCCCTG AAGGGCCTCA CCACGAGCCG GGGCGAACCG | 120 |

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|--|------|
| GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGTAC  | 180  |
| AAGGCCGTCT TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG  | 240  |
| GCCTACAAGG CGGGGAGGGC CCCGACCCCC GAGGACTTCC CCCGGCAGCT CGCCCTCATC  | 300  |
| AAGGAGCTGG TGGACCTCCT GGGGTTTACC CGCCTCGAGG TCCCCGGCTA CGAGGGGGAC  | 360  |
| GACGTTCTCG CCACCCCTGGC CAAGAAGGCG GAAAAGGAGG GGTACGAGGT GCGCATCCTC | 420  |
| ACCGCCGACC GCGACCTCTA CCAACTCGTC TCCGACCGCG TCGCCGTCCT CCACCCCGAG  | 480  |
| GGCCACCTCA TCACCCCGGA GTGGCTTTGG GAGAAGTACG GCCTCAGGCC GGAGCAGTGG  | 540  |
| GTGGACTTCC GCGCCCTCGT GGGGGACCCC TCCGACAACC TCCCCGGGGT CAAGGGCATC  | 600  |
| GGGGAGAAGA CCGCCCTCAA GCTCCTCAAG GAGTGGGGAA GCCTGGAAAA CCTCCTCAAG  | 660  |
| AACCTGGACC GGGTAAAGCC AGAAAACGTC CGGGAGAAGA TCAAGGCCA CCTGGAAGAC   | 720  |
| CTCAGGCTCT CCTTGGAGCT CTCCCGGGTG CGCACCGACC TCCCCCTGGA GGTGGACCTC  | 780  |
| GCCCAGGGGC GGGAGCCGA CGGGGAGGGG CTTAGGGCCT TCCTGGAGAG GCTGGAGTTC   | 840  |
| GGCAGCCTCC TCCACGAGTT CGGCCTCCTG GAGGCCCGG CCCCCCTGGA GGAGGCCCG    | 900  |
| TGGCCCCCGC CGGAAGGGGC CTTCGTGGGC TTCGTCCCTCT CCCGCCCGA GCCCATGTGG  | 960  |
| CGGGAGCTTA AAGCCCTGGC CGCCTGCAGG GACGGCCGGG TGCACCGGGC AGCAGACCCC  | 1020 |
| TTGGCGGGGC TAAAGGACCT CAAGGAGGTC CGGGGCCTCC TCGCCAAGGA CCTCGCCGTC  | 1080 |
| TTGGCCTCGA GGGAGGGCT AGACCTCGTG CCCGGGACG ACCCCATGCT CCTCGCCTAC    | 1140 |
| CTCCTGGACC CCTCCAACAC CACCCCGAG GGGGTGGCGC GGCGCTACGG GGGGGAGTGG   | 1200 |
| ACGGAGGACG CCGCCCACCG GGCCCTCCTC TCGGAGAGGC TCCATCGGAA CCTCCTTAAG  | 1260 |
| CGCCTCGAGG GGGAGGAGAA GCTCCTTG GCTTACACAG AGGTGGAAAA GCCCCTCTCC    | 1320 |
| CGGGTCCCTGG CCCACATGGA GGCCACCGGG GTACGGCTGG ACGTGGCCTA CCTTCAGGCC | 1380 |
| CTTCCCTGG AGCTTGCAGA GGAGATCCGC CGCCTCGAGG AGGAGGTCTT CCGCTTGGCG   | 1440 |
| GGCCACCCCT TCAACCTCAA CTCCCGGGAC CAGCTGGAAA GGGTGCTCTT TGACCGAGCTT | 1500 |
| AGGCTTCCCG CCTTGGGGAA GACGCAAAAG ACAGGCAAGC GCTCCACCAAG CGCCCGGGTG | 1560 |
| CTGGAGGCC TACGGGAGGC CCACCCATC GTGGAGAAGA TCCTCCAGCA CGGGAGCTC     | 1620 |
| ACCAAGCTCA AGAACACCTA CGTGGACCCC CTCCCAAGCC TCGTCCACCC GAGGACGGGC  | 1680 |
| CGCCTCCACA CCCGCTTCAA CCAGACGGCC ACGGCCACGG GGAGGCTTAG TAGCTCCGAC  | 1740 |
| CCCAACCTGC AGAACATCCC CGTCCGCACC CCCTTGGGCC AGAGGATCCG CGGGCCTTC   | 1800 |
| GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCCGTC   | 1860 |
| CTCGCCCACC TCTCCGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC   | 1920 |
| CACACCCAGA CCGCAAGCTG GATGTTCGGC GTCCCCCGG AGGCCGTGGA CCCCCCTGATG  | 1980 |

CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC 2040  
 TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA 2100  
 GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCCCTGGA GGAGGGGAGG AAGCGGGGCT 2160  
 ACGTGGAAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA 2220  
 GCGTCAGGGA GGCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG 2280  
 ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCCGCCT CCGGGAGATG GGGGCCCCGA 2340  
 TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG 2400  
 TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG 2460  
 TGGAGGTGGG GATGGGGAG GACTGGCTTT CCGCCAAGGG TTAG 2504

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 832 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Gly | Met | Leu | Pro | Leu | Phe | Glu | Pro | Lys | Gly | Arg | Val | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Asp | Gly | His | His | Leu | Ala | Tyr | Arg | Thr | Phe | His | Ala | Leu | Lys | Gly |
|     |     |     |     |     | 20  |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Thr | Thr | Ser | Arg | Gly | Glu | Pro | Val | Gln | Ala | Val | Tyr | Gly | Phe | Ala |
|     |     |     |     | 35  |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Lys | Ser | Leu | Leu | Lys | Ala | Leu | Lys | Glu | Asp | Gly | Asp | Ala | Val | Ile | Val |
|     |     |     |     | 50  |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Phe | Asp | Ala | Lys | Ala | Pro | Ser | Phe | Arg | His | Glu | Ala | Tyr | Gly |     |
|     | 65  |     |     |     | 70  |     |     | 75  |     |     | 80  |     |     |     |     |
| Tyr | Lys | Ala | Gly | Arg | Ala | Pro | Thr | Pro | Glu | Asp | Phe | Pro | Arg | Gln | Leu |
|     |     |     |     | 85  |     |     | 90  |     |     |     | 95  |     |     |     |     |
| Ala | Leu | Ile | Lys | Glu | Leu | Val | Asp | Leu | Leu | Gly | Leu | Ala | Arg | Leu | Glu |
|     |     |     |     | 100 |     | 105 |     |     |     | 110 |     |     |     |     |     |
| Val | Pro | Gly | Tyr | Glu | Ala | Asp | Asp | Val | Leu | Ala | Ser | Leu | Ala | Lys | Lys |
|     |     |     | 115 |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| Ala | Glu | Lys | Glu | Gly | Tyr | Glu | Val | Arg | Ile | Leu | Thr | Ala | Asp | Lys | Asp |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Tyr | Gln | Leu | Leu | Ser | Asp | Arg | Ile | His | Val | Leu | His | Pro | Glu | Gly |
|     |     |     | 145 |     |     | 150 |     |     |     | 155 |     |     | 160 |     |     |
| Tyr | Leu | Ile | Thr | Pro | Ala | Trp | Leu | Trp | Glu | Lys | Tyr | Gly | Leu | Arg | Pro |
|     |     |     | 165 |     |     |     | 170 |     |     |     | 175 |     |     |     |     |

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Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn  
180 185 190

Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu  
195 200 205

Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu  
210 215 220

Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys  
225 230 235 240

Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val  
245 250 255

Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe  
260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
275 280 285

Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
290 295 300

Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp  
305 310 315 320

Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro  
325 330 335

Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu  
340 345 350

Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro  
355 360 365

Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
370 375 380

Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
385 390 395 400

Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu  
405 410 415

Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg Glu  
420 425 430

Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly  
435 440 445

Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala  
450 455 460

Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His  
465 470 475 480

Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
485 490 495

Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
500 505 510

Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 630 635 640  
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
 705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg  
 725 730 735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 740 745 750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 755 760 765  
 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
 770 775 780  
 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala  
 785 790 795 800  
 Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
 805 810 815  
 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 820 825 830

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 831 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
1 5 10 15

Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu  
20 25 30

Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys  
35 40 45

Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val Val  
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr  
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val  
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala  
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp. Leu  
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr  
145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu  
165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile  
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg  
195 200 205

Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys  
210 215 220

Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu  
225 230 235 240

Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp  
245 250 255

Phe Gly Arg Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu  
260 265 270

Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu

275

280

285

Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala  
 290 295 300

Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu  
 305 310 315 320

Leu Ala Leu Ala Gly Ala Trp Glu Gly Arg Leu His Arg Ala Gln Asp  
 325 330 335

Pro Leu Arg Gly Leu Arg Asp Leu Lys Gly Val Arg Gly Ile Leu Ala  
 340 345 350

Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro  
 355 360 365

Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr  
 370 375 380

Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp  
 385 390 395 400

Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys  
 405 410 415

Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val  
 420 425 430

Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val  
 435 440 445

Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Glu Ala  
 450 455 460

Glu Val Arg Gln Leu Glu Glu Val Phe Arg Leu Ala Gly His Pro  
 465 470 475 480

Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu  
 485 490 495

Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser  
 500 505 510

Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val  
 515 520 525

Asp Arg Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr  
 530 535 540

Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Gly Arg Leu His  
 545 550 555 560

Thr Arg Phe Asn Gln Thr Ala Thr Gly Arg Leu Ser Ser Ser  
 565 570 575

Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg  
 580 585 590

Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Val Leu Val Val Leu  
 595 600 605

Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp  
 610 615 620  
 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Gln  
 625 630 635 640  
 Thr Ala Ser Trp Met Phe Gly Val Ser Pro Glu Gly Val Asp Pro Leu  
 645 650 655  
 Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met  
 660 665 670  
 Ser Ala His Arg Leu Ser Gly Glu Leu Ser Ile Pro Tyr Glu Glu Ala  
 675 680 685  
 Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg Ala  
 690 695 700  
 Trp Ile Glu Gly Thr Leu Glu Glu Gly Arg Arg Gly Tyr Val Glu  
 705 710 715 720  
 Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val  
 725 730 735  
 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val  
 740 745 750  
 Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Arg Leu Phe  
 755 760 765  
 Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His Asp  
 770 775 780  
 Glu Leu Val Leu Glu Ala Pro Lys Asp Arg Ala Glu Arg Val Ala Ala  
 785 790 795 800  
 Leu Ala Lys Glu Val Met Glu Gly Val Trp Pro Leu Gln Val Pro Leu  
 805 810 815  
 Glu Val Glu Val Gly Leu Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 820 825 830

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 834 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
 1 5 10 15  
 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
 20 25 30  
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
 35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
 65 70 75 80  
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg  
 130 135 140  
 Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu  
 145 150 155 160  
 Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu  
 195 200 205  
 Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp  
 225 230 235 . 240  
 Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg  
 260 265 270  
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285  
 Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300  
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp  
 305 310 315 320  
 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg  
 325 330 335  
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350  
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365  
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380

Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
385 390 395 400

Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
420 425 430

His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
435 440 445

Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
450 455 460

Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Val Phe Arg Leu Ala  
465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
485 490 495

Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly  
500 505 510

Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
515 520 525

Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
530 535 540

Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
565 570 575

Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
595 600 605

Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
625 630 635 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
645 650 655

Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
660 665 670

Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
675 680 685

Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
690 695 700

Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
705 710 715 720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Asn  
 725 730 735  
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
 770 775 780  
 Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
 785 790 795 800  
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
 805 810 815  
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
 820 825 830  
 Lys Gly

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2502 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|            |             |            |             |            |            |     |
|------------|-------------|------------|-------------|------------|------------|-----|
| ATGNNGGCGA | TGCTTCCCT   | CTTGAGCCC  | AAAGGCCGGG  | TCCTCCTGGT | GGACGGCCAC | 60  |
| CACCTGGCCT | ACCGCACCTT  | CTTCGCCCTG | AAGGCCTCA   | CCACCAGCCG | GGCGAACCG  | 120 |
| GTGCAGGCGG | TCTACGGCTT  | CGCCAAGAGC | CTCCTCAAGG  | CCCTGAAGGA | GGACGGGGAC | 180 |
| NNGGCGGTGN | TCGTGGTCTT  | TGACGCCAAG | GCCCCCTCCT  | TCCGCCACGA | GGCCTACGAG | 240 |
| GCCTACAAGG | CGGGCCGGGC  | CCCCACCCCG | GAGGACTTTTC | CCCGGCAGCT | CGCCCTCATC | 300 |
| AAGGAGCTGG | TGGACCTCCT  | GGGGCTTGCG | CGCCTCGAGG  | TCCCCGGCTA | CGAGGCGGAC | 360 |
| GACGTNCTGG | CCACCCCTGGC | CAAGAAGGCG | GAAAAGGAGG  | GGTACGAGGT | GCGCATCCTC | 420 |
| ACCGCCGACC | GCGACCTCTA  | CCAGCTCCTT | TCCGACCGCA  | TCGCCGTCT  | CCACCCCGAG | 480 |
| GGGTACCTCA | TCACCCCGGC  | GTGGCTTGG  | GAGAAGTACG  | GCCTGAGGCC | GGAGCAGTGG | 540 |
| GTGGACTACC | GGGCCCTGGC  | GGGGGACCCC | TCCGACAACC  | TCCCCGGGGT | CAAGGGCATC | 600 |
| GGGGAGAAGA | CCGCCNGAA   | GCTCCTCNAG | GAGTGGGGGA  | GCCTGGAAAA | CCTCCTCAAG | 660 |
| AACCTGGACC | GGGTGAAGCC  | CGCCNTCCGG | GAGAAGATCC  | AGGCCCACAT | GGANGACCTG | 720 |
| ANGCTCTCCT | GGGAGCTNTC  | CCAGGTGGCG | ACCGACCTGC  | CCCTGGAGGT | GGACTTCGCC | 780 |
| AAGNGGCGGG | AGCCCGACCG  | GGAGGGCTT  | AGGGCCTTTC  | TGGAGAGGCT | GGAGTTGGC  | 840 |

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|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| AGCCTCCTCC | ACGAGTTCGG  | CCTCCTGGAG  | GGCCCCAAGG  | CCCTGGAGGA  | GGCCCCCTGG  | 900  |
| CCCCCGCCGG | AAGGGGCCTT  | CGTGGGCTTT  | GTCCTTCTCC  | GCCCCGAGCC  | CATGTGGGCC  | 960  |
| GAGCTTCTGG | CCCTGGCCGC  | CGCCAGGGAG  | GGCCGGGTCC  | ACCGGGCACCC | AGACCCCTTT  | 1020 |
| ANGGGCCTNA | GGGACCTNAA  | GGAGGTGCGG  | GGNCTCCTCG  | CCAAGGACCT  | GGCCGTTTG   | 1080 |
| GCCCTGAGGG | AGGGCCTNGA  | CCTCNTGCC   | GGGGACGACC  | CCATGCTCCT  | CGCCTACCTC  | 1140 |
| CTGGACCCCT | CCAACACCAAC | CCCCGAGGGG  | GTGGCCCGGC  | GCTACGGGGG  | GGAGTGGACG  | 1200 |
| GAGGANGCGG | GGGAGCGGGC  | CCTCCTNTCC  | GAGAGGCTCT  | TCCNGAACCT  | NNNGCAGCGC  | 1260 |
| CTTGAGGGGG | AGGAGAGGCT  | CCTTTGGCTT  | TACCAAGGAGG | TGGAGAAGCC  | CCTTTCCCAG  | 1320 |
| GTCCTGGCCC | ACATGGAGGC  | CACGGGGTN   | CGGCTGGACG  | TGGCCTACCT  | CCAGGCCCTN  | 1380 |
| TCCCTGGAGG | TGGCGGAGGA  | GATCCGCCGC  | CTCGAGGAGG  | AGGTCTTCCG  | CCTGGCCGGC  | 1440 |
| CACCCCTTCA | ACCTCAACTC  | CCGGGACCAG  | CTGGAAAGGG  | TGCTCTTTGA  | CGAGCTNGGG  | 1500 |
| CTTCCCGCCA | TCGGCAAGAC  | GGAGAAAGACN | GGCAAGCGCT  | CCACCAGCGC  | CGCCGTGCTG  | 1560 |
| GAGGCCCTNC | GNGAGGCCA   | CCCCATCGTG  | GAGAAGATCC  | TGCAGTACCG  | GGAGCTCAC   | 1620 |
| AAGCTCAAGA | ACACCTACAT  | NGACCCCCCTG | CCNGNCCTCG  | TCCACCCAG   | GACGGGCCGC  | 1680 |
| CTCCACACCC | GCTTCAACCA  | GACGGCCACG  | GCCACGGCA   | GGCTTAGTAG  | CTCCGACCCC  | 1740 |
| AACCTGCAGA | ACATCCCCGT  | CCGCACCCCN  | CTGGGCCAGA  | GGATCCGCCG  | GGCCTTCGTG  | 1800 |
| GCCGAGGAGG | GNTGGGTGTT  | GGTGGCCCTG  | GACTATAGCC  | AGATAGAGCT  | CCGGGTCCCTG | 1860 |
| GCCCACCTCT | CCGGGGACGA  | GAACCTGATC  | CGGGTCTTCC  | AGGAGGGGAG  | GGACATCCAC  | 1920 |
| ACCCAGACCG | CCAGCTGGAT  | GTTCGCGTC   | CCCCCGGAGG  | CCGTGGACCC  | CCTGATGCGC  | 1980 |
| CGGGCGGCCA | AGACCATCAA  | CTTCGGGGTC  | CTCTACGGCA  | TGTCCGCCA   | CCGCCTCTCC  | 2040 |
| CAGGAGCTTG | CCATCCCCTA  | CGAGGAGGCG  | GTGGCCTTCA  | TTGAGCGCTA  | CTTCCAGAGC  | 2100 |
| TTCCCCAAGG | TGCGGGCTG   | GATTGAGAAG  | ACCTGGAGG   | AGGGCAGGAG  | GGGGGGGTAC  | 2160 |
| GTGGAGACCC | TCTTCGGCCG  | CCGGCGCTAC  | GTGCCCGACC  | TCAACGCCCG  | GGTGAAGAGC  | 2220 |
| GTGCGGGAGG | CGGCGGAGCG  | CATGGCCTTC  | AACATGCCCG  | TCCAGGGCAC  | CGCCGCCGAC  | 2280 |
| CTCATGAAGC | TGGCCATGGT  | GAAGCTCTTC  | CCCCGGCTNC  | AGGAAATGGG  | GGCCAGGATG  | 2340 |
| CTCCTNCAGG | TCCACGACGA  | GCTGGTCCTC  | GAGGGCCCCA  | AAGAGCGGGC  | GGAGGNGGTG  | 2400 |
| GCCGCTTTGG | CCAAGGAGGT  | CATGGAGGGG  | GTCTATCCCC  | TGGCCGTGCC  | CCTGGAGGTG  | 2460 |
| GAGGTGGGGA | TGGGGGAGGA  | CTGGCTCTCC  | GCCAAGGAGT  | AG          |             | 2502 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 833 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Xaa Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu  
1 5 10 15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly  
20 25 30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala  
35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val  
50 55 60

Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala  
65 70 75 80

Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu  
85 90 95

Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu  
100 105 110

Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys  
115 120 125

Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp  
130 135 140

Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly  
145 150 155 160

Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro  
165 170 175

Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn  
180 185 190

Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu  
195 200 205

Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val  
210 215 220

Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa  
225 230 235 240

Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val  
245 250 255

Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe  
260 265 270

Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
275 280 285

Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
290 295 300

Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320  
 Leu Leu Ala Leu Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa  
 325 330 335  
 Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu  
 405 410 415  
 Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala  
 450 455 460  
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
 625 630 635 640

Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro  
                   645                     650                     655  
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
                   660                     665                     670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
                   675                     680                     685  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
                   690                     695                     700  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
                   705                     710                     715                     720  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg  
                   725                     730                     735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
                   740                     745                     750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
                   755                     760                     765  
 Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
                   770                     775                     780  
 Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala  
                   785                     790                     795                     800  
 Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
                   805                     810                     815  
 Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu  
                   820                     825                     830  
 Xaa

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1647 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|  |     |
|--|-----|
| ATGAATTCTGG GGATGCTGCC CCTCTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC  | 60  |
| CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAAG CCGGGGGGAG | 120 |
| CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG  | 180 |
| GACGCCGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG  | 240 |
| GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC  | 300 |
| AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC  | 360 |

|             |             |            |            |            |            |      |
|-------------|-------------|------------|------------|------------|------------|------|
| GACGTCTGG   | CCAGCCTGGC  | CAAGAAGGCG | GAAAAGGAGG | GCTACGAGGT | CCGCATCCTC | 420  |
| ACCGCCGACA  | AAGACCTTTA  | CCAGCTCCTT | TCCGACCGCA | TCCACGTCCT | CCACCCCGAG | 480  |
| GGGTACCTCA  | TCACCCCCGGC | CTGGCTTTGG | GAAAAGTACG | GCCTGAGGCC | CGACCAGTGG | 540  |
| GCCGACTACC  | GGGCCCTGAC  | CGGGGACGAG | TCCGACAACC | TTCCCGGGGT | CAAGGGCATC | 600  |
| GGGGAGAAGA  | CGGCGAGGAA  | GCTTCTGGAG | GAGTGGGGGA | GCCTGGAAGC | CCTCCTCAAG | 660  |
| AACCTGGACC  | GGCTGAAGCC  | CGCCATCCGG | GAGAAGATCC | TGGCCCACAT | GGACGATCTG | 720  |
| AAGCTCTCCT  | GGGACCTGGC  | CAAGGTGCGC | ACCGACCTGC | CCCTGGAGGT | GGACTTCGCC | 780  |
| AAAAGGCGGG  | AGCCCGACCG  | GGAGAGGCTT | AGGGCCTTTC | TGGAGAGGCT | TGAGTTTGGC | 840  |
| AGCCTCCTCC  | ACGAGTTCGG  | CCTTCTGGAA | AGCCCCAAGG | CCCTGGAGGA | GGCCCCCTGG | 900  |
| CCCCCGCCGG  | AAGGGGCCTT  | CGTGGGCTTT | GTGCTTCCC  | GCAAGGAGCC | CATGTGGGCC | 960  |
| GATCTTCTGG  | CCCTGGCCGC  | CGCCAGGGGG | GGCCGGGTCC | ACCGGGCCCC | CGAGCCTTAT | 1020 |
| AAAGCCCTCA  | GGGACCTGAA  | GGAGGCGCGG | GGGCTTCTCG | CCAAAGACCT | GAGCGTTCTG | 1080 |
| GCCCTGAGGG  | AAGGCCTTGG  | CCTCCCGCCC | GGCGACGACC | CCATGCTCCT | CGCCTACCTC | 1140 |
| CTGGACCCCTT | CCAACACCAAC | CCCCGAGGGG | GTGGCCCGGC | GCTACGGCGG | GGAGTGGACG | 1200 |
| GAGGAGGCAG  | GGGAGCGGGC  | CGCCCTTTCC | GAGAGGCTCT | TCGCCAACCT | GTGGGGGAGG | 1260 |
| CTTGAGGGGG  | AGGAGAGGCT  | CCTTTGGCTT | TACCGGGAGG | TGGAGAGGCC | CCTTTCCGCT | 1320 |
| GTCCTGGCCC  | ACATGGAGGC  | CACGGGGGTG | CGCCTGGACG | TGGCCTATCT | CAGGGCCTTG | 1380 |
| TCCCTGGAGG  | TGGCCGGGA   | GATCGCCCGC | CTCGAGGCCG | AGGTCTTCCG | CCTGGCCGGC | 1440 |
| CACCCCTTCA  | ACCTCAACTC  | CCGGGACCAG | CTGGAAAGGG | TCCTCTTTGA | CGAGCTAGGG | 1500 |
| CTTCCCGCCA  | TCGGCAAGAC  | GGAGAAGACC | GGCAAGCGCT | CCACCAGCGC | CGCCGTCTG  | 1560 |
| GAGGCCCTCC  | GCGAGGCCCA  | CCCCATCGTG | GAGAAGATCC | TGCAGGCATG | CAAGCTTGGC | 1620 |
| ACTGGCCGTC  | GTTTACAAC   | GTCTGTGA   |            |            |            | 1647 |

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2088 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|             |            |            |            |             |             |     |
|-------------|------------|------------|------------|-------------|-------------|-----|
| ATGAATTCTGG | GGATGCTGCC | CCTCTTTGAG | CCCAAGGGCC | GGGTCCCTCCT | GGTGGACGGC  | 60  |
| CACCAACCTGG | CCTACCGCAC | CTTCCACGCC | CTGAAGGGCC | TCACCACCAAG | CCGGGGGGAG  | 120 |
| CCGGTGCAGG  | CGGTCTACGG | CTTCGCCAAG | AGCCTCCTCA | AGGCCCTCAA  | GGAGGGACGGG | 180 |

GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG 240  
GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGAATTTC CCCGGCAACT CGCCCTCATC 300  
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCAGGCTA CGAGGCGGAC 360  
GACGTCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC 420  
ACCGCCGACA AAGACCTTA CCAGCTCCTT TCCGACCGCA TCCACGTCTT CCACCCCGAG 480  
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG 540  
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC 600  
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG 660  
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG 720  
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC 780  
AAAAGGCGGG AGCCCGACCG GGAGAGGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTGGC 840  
AGCCTCCTCC ACGAGTTCGG CCTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG 900  
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTGCTTTCCC GCAAGGAGCC CATGTGGGCC 960  
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCC CGAGCCTTAT 1020  
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG 1080  
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GGCGACGACC CCATGCTCCT CGCCTACCTC 1140  
CTGGACCCCTT CCAACACCAAC CCCCAGGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG 1200  
GAGGAGGCGG GGGAGCGGGC CGCCCTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG 1260  
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTTCCGCT 1320  
GTCCTGGCCC ACATGGAGGC CACGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG 1380  
TCCCTGGAGG TGGCCGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC 1440  
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TCCTCTTGA CGAGCTAGGG 1500  
CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCTG 1560  
GAGGCCCTCC GCGAGGCCA CCCCACCGTG GAGAAGATCC TGCAGTACCG GGAGCTCACC 1620  
AAGCTGAAGA GCACCTACAT TGACCCCTTG CCGGACCTCA TCCACCCAG GACGGGCCGC 1680  
CTCCACACCC GCTTCAACCA GACGGCCACG GCCACGGGCA GGCTAAGTAG CTCCGATCCC 1740  
AACCTCCAGA ACATCCCCGT CCGCACCCCG CTTGGGCAGA GGATCCGCCG GGCCCTCATC 1800  
GCCGAGGAGG GGTGGCTATT GGTGGCCTG GACTATAGCC AGATAGAGCT CAGGGTGTCTG 1860  
GCCCACCTCT CCGGCGACGA GAACCTGATC CGGGTCTTCC AGGAGGGCGG GGACATCCAC 1920  
ACGGAGACCG CCAGCTGGAT GTTCGGCGTC CCCCAGGGAGG CGTGGACCC CCTGATGCC 1980  
CGGGCGGCCA AGACCATCAA CTTCGGGTC CTCTACGGCA TGTCGGCCCA CGGCCTCTCC 2040

CAGGAGCTAG CTAGCCATCC CTTACGAGGA GGCCCAGGCC TTCATTGA

2088

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 962 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|  |     |
|--|-----|
| ATGAATTCTGG GGATGCTGCC CCTCTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC  | 60  |
| CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAAG CGGGGGGGAG | 120 |
| CCGGTGCAGG CGGTCTACGG CTTGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG   | 180 |
| GACGCCGTGA TCGTGGCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG   | 240 |
| GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC  | 300 |
| AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC  | 360 |
| GACGTCTGG CCAGCCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC   | 420 |
| ACCGCCGACA AAGACCTTA CCAGCTTCTT TCCGACCGCA TCCACGTCTT CCACCCGAG    | 480 |
| GGGTACCTCA TCACCCCGGC CTGGCTTGG GAAAAGTACG GCCTGAGGCC CGACCAAGTGG  | 540 |
| GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC  | 600 |
| GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG  | 660 |
| AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG  | 720 |
| AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTCGCC  | 780 |
| AAAAGGCGGG AGCCCCACCG GGAGAGGCTT AGGGCTTTC TGGAGAGGCT TGAGTTGGC    | 840 |
| AGCCTCCTCC ACGAGTTGG CTTCTGGAA AGCCCCAAGT CATGGAGGGG GTGTATCCCC    | 900 |
| TGGCCGTGCC CCTGGAGGTG GAGGTGGGG TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT   | 960 |
| GA   | 962 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1600 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|   |    |
|---|----|
| ATGGAATTCTG GGGATGCTGC CCCTCTTGA GCCCAAGGGC CGGGTCCTCC TGGTGGACGG | 60 |
|---|----|

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|--|------|
| CCACCACTG GCCTACCGA CCTTCCACGC CCTGAAGGGC CTCACCACCA GCCGGGGGGA    | 120  |
| GCCGGTGCAG GCGGTCTACG GCTTCGCCAA GAGCCTCCTC AAGGCCCTCA AGGAGGACGG  | 180  |
| GGACGGGTG ATCGTGGTCT TTGACGCCAA GGCCCCCTCC TTCCGCCACG AGGCCTACGG   | 240  |
| GGGGTACAAG CGGGGCCGGG CCCCCACGCC GGAGGACTTT CCCCGGCAAC TCGCCCTCAT  | 300  |
| CAAGGAGCTG GTGGACCTCC TGGGCTGGC GCGCCTCGAG GTCCCAGGCT ACGAGGCGGA   | 360  |
| CGACGTCCTG GCCAGCCTGG CCAAGAAGGC GGAAAAGGAG GGCTACGAGG TCCGCATCCT  | 420  |
| CACCGCCGAC AAAGACCTTT ACCAGCTCCT TTCCGACCGC ATCCACGTCC TCCACCCGA   | 480  |
| GGGGTACCTC ATCACCCGG CCTGGCTTTG GGAAAAGTAC GGCCTGAGGC CCGACCAGTG   | 540  |
| GGCCGACTAC CGGGCCCTGA CGGGGGACGA GTCCGACAAC CTTCCCGGGG TCAAGGGCAT  | 600  |
| CGGGGAGAAG ACGGCGAGGA AGCTTCTGGA GGAGTGGGGG AGCCTGGAAG CCCTCCTCAA  | 660  |
| GAACCTGGAC CGGCTGAAGC CCGCCATCCG GGAGAAGATC CTGGCCCACA TGGACGATCT  | 720  |
| GAAGCTCTCC TGGGACCTGG CCAAGGTGCG CACCGACCTG CCCCTGGAGG TGGACTTCGC  | 780  |
| CAAAAGGCGG GAGCCCGACC GGGAGAGGCT TAGGGCCTTT CTGGAGAGGC TTGAGTTGG   | 840  |
| CAGCCTCCTC CACGAGTTCG GCCTTCTGGA AAGCCCCAAG ATCCGCCGGG CCTTCATCGC  | 900  |
| CGAGGAGGGG TGGCTATTGG TGGCCCTGGA CTATAGCCAG ATAGAGCTCA GGGTGCTGGC  | 960  |
| CCACCTCTCC GGCGACGAGA ACCTGATCCG GGTCTTCAG GAGGGCGGG ACATCCACAC    | 1020 |
| GGAGACCGCC AGCTGGATGT TCGGCGTCCC CGGGGAGGCC GTGGACCCCC TGATGCGCCG  | 1080 |
| GGCGGCCAAG ACCATCAACT TCGGGGTCCCT CTACGGCATG TCGGCCACC GCCTCTCCCA  | 1140 |
| GGAGCTAGCC ATCCCTTACG AGGAGGCCA GGCTTCATT GAGCGCTACT TTCAGAGCTT    | 1200 |
| CCCCAAGGTG CGGGCCTGGA TTGAGAAGAC CCTGGAGGAG GGCAGGAGGC GGGGGTACGT  | 1260 |
| GGAGACCCCTC TTCGGCCGCC GCCGCTACGT GCCAGACCTA GAGGCCCGGG TGAAGAGCGT | 1320 |
| GCGGGAGGGG GCCGAGCGCA TGGCCTTCAA CATGCCCGTC CGGGGCACCG CCGCCGACCT  | 1380 |
| CATGAAGCTG GCTATGGTGA AGCTCTTCCC CAGGCTGGAG GAAATGGGGG CCAGGATGCT  | 1440 |
| CCTTCAGGTC CACGACGAGC TGGTCCTCGA GGCCCCAAAA GAGAGGGCGG AGGCCGTGGC  | 1500 |
| CCGGCTGGCC AAGGAGGTCA TGGAGGGGGT GTATCCCTG GCCGTGCCCG TGGAGGTGGA   | 1560 |
| GGTGGGGATA GGGGAGGACT GGCTCTCCGC CAAGGAGTGA                        | 1600 |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACGAATTCTG GGGATGCTGC CCCTCTTG GA GCCCAA

36

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAGATCTA TCACTCCTTG GCGGAGAGCC AGTC

34

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 91 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAGCTCGC CCGGGCGAGC TCGAATTCCG

60

TGTATTCTAT AGTGTACCT AAATCGAATT C

91

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGATT TAGGTGACAC TATAGAA

27

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAATCATGG TCATAGCTGG TAGCTTGCTA C

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCCTCTA GAGTCGACCT GCAGGCATGC CTACCTTGGT AG

42

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATCCTCTA GAGTCGACCT GCAGGCATGC

30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2502 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAATTCTGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC

60

CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAAG CCGGGGGGAG

120

CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGGACGGG

180

GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG

240

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|             |             |             |            |            |            |      |
|-------------|-------------|-------------|------------|------------|------------|------|
| GGGTACAAGG  | CGGGCCGGGC  | CCCCACGCCG  | GAGGACTTTC | CCCGGCAACT | CGCCCTCATC | 300  |
| AAGGAGCTGG  | TGGACCTCCT  | GGGGCTGGCG  | CGCCTCGAGG | TCCCAGGCTA | CGAGGCGGAC | 360  |
| GACGTCTGG   | CCAGCCTGGC  | CAAGAACCGG  | GAAAAGGAGG | GCTACGAGGT | CCGCATCCTC | 420  |
| ACCGCCGACA  | AAGACCTTTA  | CCAGCTCCTT  | TCCGACCGCA | TCCACGTCT  | CCACCCCGAG | 480  |
| GGGTACCTCA  | TCACCCCGC   | CTGGCTTTGG  | GAAAAGTACG | GCCTGAGGCC | CGACCAGTGG | 540  |
| GCCGACTACC  | GGGCCCTGAC  | CGGGGACGAG  | TCCGACAACC | TTCCCAGGGT | CAAGGGCATC | 600  |
| GGGGAGAAGA  | CGGCGAGGAA  | GCTTCTGGAG  | GAGTGGGGGA | GCCTGGAAGC | CCTCCTCAAG | 660  |
| AACCTGGACC  | GGCTGAAGCC  | CGCCATCCGG  | GAGAAGATCC | TGGCCCACAT | GGACGATCTG | 720  |
| AAGCTCTCCT  | GGGACCTGGC  | CAAGGTGCGC  | ACCGACCTGC | CCCTGGAGGT | GGACTTCGCC | 780  |
| AAAAGGCGGG  | AGCCCGACCG  | GGAGAGGGCTT | AGGGCCTTTC | TGGAGAGGCT | TGAGTTGGC  | 840  |
| AGCCTCCTCC  | ACGAGTTCGG  | CCTTCTGGAA  | AGCCCCAAGG | CCCTGGAGGA | GGCCCCCTGG | 900  |
| CCCCCGCCGG  | AAGGGGCCTT  | CGTGGGCTTT  | GTGCTTCCC  | GCAAGGAGCC | CATGTGGGCC | 960  |
| GATCTTCTGG  | CCCTGGCCGC  | CGCCAGGGGG  | GGCCGGGTCC | ACCGGGCCCC | CGAGCCTTAT | 1020 |
| AAAGCCCTCA  | GGGACCTGAA  | GGAGGCGCGG  | GGGCTTCTCG | CCAAAGACCT | GAGCGTTCTG | 1080 |
| GCCCTGAGGG  | AAGGCCTTGG  | CCTCCCGCCC  | GGCGACGACC | CCATGCTCCT | CGCCTACCTC | 1140 |
| CTGGACCCCTT | CCAACACCAAC | CCCCGAGGGG  | GTGGCCCGC  | GCTACGGCGG | GGAGTGGACG | 1200 |
| GAGGAGGCGG  | GGGAGCGGGC  | CGCCCTTCC   | GAGAGGCTCT | TCGCCAACCT | GTGGGGAGG  | 1260 |
| CTTGAGGGGG  | AGGAGAGGCT  | CCTTGGCTT   | TACCGGGAGG | TGGAGAGGCC | CCTTCCGCT  | 1320 |
| GTCCTGGCCC  | ACATGGAGGC  | CACGGGGGTG  | CGCCTGGACG | TGGCCTATCT | CAGGGCCTTG | 1380 |
| TCCCTGGAGG  | TGGCCGGGA   | GATGCCCGC   | CTCGAGGCCG | AGGTCTTCCG | CCTGGCCGGC | 1440 |
| CACCCCTTCA  | ACCTCAACTC  | CCGGGACCAAG | CTGGAAAGGG | TCCTCTTGA  | CGAGCTAGGG | 1500 |
| CTTCCCGCCA  | TCGGCAAGAC  | GGAGAAGACC  | GGCAAGCGCT | CCACCAGCGC | CGCCGTCTG  | 1560 |
| GAGGCCCTCC  | GCGAGGCCA   | CCCCATCGTG  | GAGAAGATCC | TGCAGTACCG | GGAGCTCAC  | 1620 |
| AAGCTGAAGA  | GCACCTACAT  | TGACCCCTTG  | CCGGACCTCA | TCCACCCAG  | GACGGGCCGC | 1680 |
| CTCCACACCC  | GCTCAACCA   | GACGGCCACG  | GCCACGGCA  | GGCTAAGTAG | CTCCGATCCC | 1740 |
| AACCTCCAGA  | ACATCCCCGT  | CCGCACCCCG  | CTTGGGCAGA | GGATCCGCCG | GGCCCTCATC | 1800 |
| GCCGAGGAGG  | GGTGGCTATT  | GGTGGCCCTG  | GAATATGCC  | AGATAGAGCT | CAGGGTGCTG | 1860 |
| GCCCACCTCT  | CGGGCGACGA  | GAACCTGATC  | CGGGCTTCC  | AGGAGGGCG  | GGACATCCAC | 1920 |
| ACGGAGACCG  | CCAGCTGGAT  | GTTCGGCGTC  | CCCCGGGAGG | CCGTGGACCC | CCTGATGCGC | 1980 |
| CGGGCGGCCA  | AGACCATCAA  | CTTCGGGGTC  | CTCTACGGCA | TGTCGGCCCA | CCGCCTCTCC | 2040 |
| CAGGAGCTAG  | CCATCCCTTA  | CGAGGAGGCC  | CAGGCCTTCA | TTGAGCGCTA | CTTCAGAGC  | 2100 |

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| TTCCCCAAGG  | TGCGGGCCTG | GATTGAGAAG | ACCCTGGAGG | AGGGCAGGAG | GCGGGGTAC  | 2160 |
| GTGGAGACCC  | TCTTCGGCCG | CCGCCGCTAC | GTGCCAGACC | TAGAGGCCCG | GGTGAAGAGC | 2220 |
| GTGCGGGAGG  | C GGCGAGCG | CATGGCCTTC | AACATGCCCG | TCCGGGGCAC | CGCCGCCGAC | 2280 |
| CTCATGAAGC  | TGGCTATGGT | GAAGCTCTTC | CCCAGGCTGG | AGGAAATGGG | GGCCAGGATG | 2340 |
| CTCCTTCAGG  | TCCACGACGA | GCTGGTCCTC | GAGGCCCAA  | AAGAGAGGGC | GGAGGCCGTG | 2400 |
| GCCCCGGCTGG | CCAAGGAGGT | CATGGAGGGG | GTGTATCCCC | TGGCCGTGCC | CCTGGAGGTG | 2460 |
| GAGGTGGGGA  | TAGGGGAGGA | CTGGCTCTCC | GCCAAGGAGT | GA         |            | 2502 |

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|           |           |    |
|-----------|-----------|----|
| GATTAGGTG | ACACTATAG | 19 |
|-----------|-----------|----|

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 72 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|            |            |            |            |            |            |    |
|------------|------------|------------|------------|------------|------------|----|
| CGGACGAACA | AGCGAGACAG | CGACACAGGT | ACCACATGGT | ACAAGAGGCA | AGAGAGACGA | 60 |
|------------|------------|------------|------------|------------|------------|----|

|            |    |    |
|------------|----|----|
| CACAGCAGAA | AC | 72 |
|------------|----|----|

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 70 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|            |           |           |            |            |            |    |
|------------|-----------|-----------|------------|------------|------------|----|
| GTTCCTGCTG | TGTCGTCCT | CTTGCTCTT | GTACCATGTG | GTACCTGTGT | CGCTGTCTCG | 60 |
|------------|-----------|-----------|------------|------------|------------|----|

|            |  |  |  |  |  |    |
|------------|--|--|--|--|--|----|
| CTTGTTCGTC |  |  |  |  |  | 70 |
|------------|--|--|--|--|--|----|

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACGAACAAG CGAGACAGCG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTTCTGCTG TGTCGTCTCT CTTG

24

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTTGATAC CATGTGGTAC CTGTGTCGCT GTCTCGCTTG TTCGTC

46

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACACAGGTAC CACATGGTAC AAGAGGCAAG AGAGACGACA CAGCAGAAAC

50

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

|  |     |
|--|-----|
| ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTGGGGAT GCTGCCCTC    | 60  |
| TTTGAGCCA AGGGCCGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC    | 120 |
| CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC  | 180 |
| GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTIGAC  | 240 |
| GCCAAGGCC CCCTCCTCCG CCACGAGGCC TACGGGGGT ACAAGGCGGG CCGGGCCCCC    | 300 |
| ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG  | 360 |
| CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG  | 420 |
| AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTATTACAG | 480 |
| CTTCTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG   | 540 |
| CTTTGGGAAA AGTACGGCCT GAGGCCGCAC CAGTGGGCCG ACTACCGGGC CCTGACCGGG  | 600 |
| GACGAGTCGG ACAACCTTCC CGGGGTCAAG GGCATCGGG AGAAGACGGC GAGGAAGCTT   | 660 |
| CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACCT GGACCGGCT GAAGCCCGCC  | 720 |
| ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG  | 780 |
| GTGCGCACCG ACCTGCCCT GGAGGTGGAC TTCGCCAAAA GGCGGGAGCC CGACCGGGAG   | 840 |
| AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT  | 900 |
| CTGGAAAGCC CCAAGTCATG GAGGGGGTGT ATCCCCCTGGC CGTGCCCTG GAGGTGGAGG  | 960 |
| TGGGGATAG  | 969 |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

|   |     |
|---|-----|
| ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTGGGGAT GCTGCCCTC   | 60  |
| TTTGAGCCA AGGGCCGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC   | 120 |
| CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC | 180 |
| GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTGAC  | 240 |
| GCCAAGGCC CCTCCTTCCG CCACGAGGCC TACGGGGGT ACAAGGCGGG CCGGGCCCCC   | 300 |
| ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG | 360 |
| CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG | 420 |
| AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG | 480 |
| CTTCTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG  | 540 |
| CTTTGGGAAA AGTACGGCCT GAGGCCGCAG CAGTGGCCG ACTACCGGGC CCTGACCGGG  | 600 |
| GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATGGGG AGAACGAGGC GAGGAAGCTT  | 660 |
| CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCGCC | 720 |
| ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG | 780 |
| GTGCGCACCG ACCTGCCCT GGAGGTGGAC TTCGCCAAA GGCAGGGAGCC CGACCGGGAG  | 840 |
| AGGCTTAGGG CCTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT  | 900 |
| CTGGAAAGCC CCAAGGCCGC ACTCGAGCAC CACCACCAACC ACCACTGA             | 948 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

|   |     |
|---|-----|
| CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT | 60  |
| CACTATAGGG CGAATTGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT  | 120 |
| GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG | 180 |
| TTCCCTGTGT GAAATTGTTA TCCGCT                                      | 206 |

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 43 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTCTGGGTTTC TCTGCTCTCT GGTCGCTGTC TCGCTTGTTC GTC

43

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCTGTCTCGC TTGTTCGTC

19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GACGAACAAG CGAGACAGCG

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCTGGGTTTC TCTGCTCTCT GGTC

24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA

43

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCAGAGAGC AGAGAACCCA GAA

23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AACAGCTATG ACCATGATTA C

21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCA

157

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG

157

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CACCGTCCTC TTCAAGAAG

19

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTGAATCTTG TAGATAGCTA

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCCTTATTAACTTTCAAAATG TTTCTTTAT ACACAATATG TTTCTTAGTC

60

TGAATAACCT TTTCCTCTGC AGTATTTTG ACCAGTGGCT CCGAAGGCAC CGTCCTCTTC

120

AAGAAGTTTA TCCAGAAGGCC AATGCACCCA TTAGACATAA CCGGGAAATCC TACATGGTTC

180

CTTTTATACC ACTGTACAGA AATGGTGATT TCTTTATTTTC ATCCAAAGAT CTGGGCTATG

240

ACTATAGCTA TCTACAAAGAT TCAGGTAAAG TTTACTTTCT TTCAGAGGAA TTGCTGAATC

300

TAGTGTACC AATTTATTTT GAGATAACAC AAAACTTTA

339

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCCTTATTTC ACTTTAAAAA T

21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAAGTTTG TGTTATCTCA

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCA

157

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC

60

CATTTCGTAA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CCAATGGGTG

120

CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG

157

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

D  
O  
C  
E  
N  
T  
W  
I  
D  
B  
D  
P

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|   |     |
|---|-----|
| AGCGGATAAC AATTCACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTATTTAGG  | 60  |
| TGACACTATA GAATACTCAA GCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCCCGGGT | 120 |
| ACCGAGCTCG AATTGCCCT ATAGTGAGTC GTATTAGGAT CCGTG                  | 165 |

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

|  |     |
|--|-----|
| CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT  | 60  |
| CACTATAGGG CGAACATCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT | 120 |
| GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG  | 180 |
| TTTCCTGTGT GAAATTGTTA TCCGCT                                       | 206 |

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

|                           |    |
|---------------------------|----|
| AGCGGATAAC AATTCACAC AGGA | 24 |
|---------------------------|----|

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

|                                 |    |
|---------------------------------|----|
| CACGGATCCT AATACGACTC ACTATAGGG | 29 |
|---------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CGCCAGGGTT TTCCCAGTCA CGAC

24

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA

60

TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAAG

157

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA

60

TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA

120

GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAAG

157

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 378 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA

60

|   |     |
|---|-----|
| TCCTACATGG TTCCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTAT TTCATCCAAA  | 120 |
| GATCTGGCCT ATGACTATAG CTATCTACAA GATTCA GACC CAGACTCTT TCAAGACTAC | 180 |
| ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GGCGGCATG  | 240 |
| GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG | 300 |
| AGAAAGCAGC TTCTGAAGA AAAGCAGCCA CTCTCATGG AGAAAGAGGA TTACCA CAGC  | 360 |
| TTGTATCAGA GCCATTAA   | 378 |

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 378 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

|   |     |
|---|-----|
| CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA | 60  |
| TCCTACATGG TTCCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTAT TTCATCCAAA  | 120 |
| GATCTGGCCT ATGACTATAG CTATCTACAA GATTCA GACC CAGACTCTT TCAAGACTAC | 180 |
| ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GGCGGCATG  | 240 |
| GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG | 300 |
| AGAAAGCAGC TTCTGAAGA AAAGCAGCCA CTCTCATGG AGAAAGAGGA TTACCA CAGC  | 360 |
| TTGTATCAGA GCCATTAA   | 378 |

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1059 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|   |     |
|---|-----|
| GCAAGTTTGG CTTTTGGGCA CCAAATGCA CAGAGAGACG ACTCTTGGTG AGAAGAAACA  | 60  |
| TCTTCGATTG GAGTCCCCA GAGAAGGACA AATTTTTGC CTACCTCACT TTAGCAAAGC   | 120 |
| ATACCATCAG CTCAGACTAT GTCATCCCCA TAGGGACCTA TGGCAAATG AAAATGGAT   | 180 |
| CAACACCCAT GTTTAACGAC ATCAATATTT ATGACCTCTT TGTCTGGATG CATTATTATG | 240 |
| TGTCAATGGA TGCAGTGCTT GGGGGATATG AAATCTGGAG AGACATTGAT TTTGCCATG  | 300 |
| AAGCACCAGC TTTCTGCCT TGGCATAGAC TCTTCTTGTG GCGGTGGAA CAAGAAATCC   | 360 |

|   |      |
|---|------|
| AGAAGCTGAC AGGAGATGAA AACTTCACTA TTCCATATTG GGACTGGCGG GATGCAGAAA   | 420  |
| AGTGTGACAT TTGCACAGAT GAGTACATGG GAGGTCAGCA CCCCACAAAT CCTAACTTAC   | 480  |
| TCAGCCCAGC ATCATTCTTC TCCTCTTGGC AGATTGTCTG TAGCCGATTG GAGGAGTACA   | 540  |
| ACAGCCATCA GTCTTATGC AATGGAACGC CCGAGGGACC TTTACGGCGT AATCCTGGAA    | 600  |
| ACCATGACAA ATCCAGAACCC CCAAGGCTCC CCTCTTCAGC TGATGTAGAA TTTTGCCCTGA | 660  |
| GTTTGACCCA ATATGAATCT GGTTCCATGG ATAAAGCTGC CAATTTCAGC TTTAGAAATA   | 720  |
| CACTGGAAGG ATTTGCTAGT CCACTTACTG GGATAGCGGA TGCCTCTCAA AGCAGCATGC   | 780  |
| ACAATGCCCT GCACATCTAT ATGAATGGAA CAATGTCCCCA GGTACAGGGAA TCTGCCAACG | 840  |
| ATCCTATCTT CCTTCTTCAC CATGCATTG TTGACAGTAT TTTTGAGCAG TGGCTCCGAA    | 900  |
| GGCACCGTCC TCTTCAAGAA GTTTATCCAG AAGCCAATGC ACCCATTGGA CATAACCGGG   | 960  |
| AATCCTACAT GGTTCTTTT ATACCACTGT ACAGAAATGG TGATTTCTTT ATTTCATCCA    | 1020 |
| AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCA                           | 1059 |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

|   |     |
|---|-----|
| GCAAGTTGG CTTTTGGGGA CCAAACGTGCA CAGAGAGACG ACTCTTGGTG AGAAGAAACA   | 60  |
| TCTTCGATTT GAGTGCCCA GAGAAGGACA AATTTTTGCTACACTCTACT TTAGCAAAGC     | 120 |
| ATACCATCAG CTCAGACTAT GTCATCCCCA TAGGGACCTA TGGCCAAATG AAAAATGGAT   | 180 |
| CAACACCCAT GTTTAACGAC ATCAATATTG ATGACCTCTT TGTCTGGATG CATTATTATG   | 240 |
| TGTCAATGGA TGCAGTGCTT GGGGGATATG AAATCTGGAG AGACATTGAT TTTGCCATG    | 300 |
| AAGCACCAGC TTTCTGCCT TGGCATAGAC TCTTCTTGTT GCGGTGGGAA CAAGAAATCC    | 360 |
| AGAAGCTGAC AGGAGATGAA AACTTCACTA TTCCATATTG GGACTGGCGG GATGCAGAAA   | 420 |
| AGTGTGACAT TTGCACAGAT GAGTACATGG GAGGTCAGCA CCCCACAAAT CCTAACTTAC   | 480 |
| TCAGCCCAGC ATCATTCTTC TCCTCTTGGC AGATTGTCTG TAGCCGATTG GAGGAGTACA   | 540 |
| ACAGCCATCA GTCTTATGC AATGGAACGC CCGAGGGACC TTTACGGCGT AATCCTGGAA    | 600 |
| ACCATGACAA ATCCAGAACCC CCAAGGCTCC CCTCTTCAGC TGATGTAGAA TTTTGCCCTGA | 660 |
| GTTTGACCCA ATATGAATCT GGTTCCATGG ATAAAGCTGC CAATTTCAGC TTTAGAAATA   | 720 |
| CACTGGAAGG ATTTGCTAGT CCACTTACTG GGATAGCGGA TGCCTCTCAA AGCAGCATGC   | 780 |

|  |                       |      |
|--|-----------------------|------|
| ACAATGCCTT GCACATCTAT ATGAATGGAA CAATGTCCC A                   | GGTACAGGGA TCTGCCAACG | 840  |
| ATCCTATCTT CCTTCTTCAC CATGCATTG TTGACAGTAT TTTTGAGCAG          | TGGCTCCGAA            | 900  |
| GGCACCGTCC TCTTCAAGAA GTTTATCCAG AAGCCAATGC ACCCATGG           | CATAACCAGG            | 960  |
| AATCCTACAT GGTTCTTTT ATACCACTGT ACAGAAATGG TGATTCTTT ATTCATCCA |                       | 1020 |
| AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCAG                     |                       | 1059 |

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1587 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

|  |      |
|--|------|
| ATGCTCCTGG CTGTTTGTA CTGCCTGCTG TGGAGTTCC AGACCTCCGC TGGCCATT      | 60   |
| CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC  | 120  |
| GGGGACAGGA GTCCCTGTGG CCAGCTTCA GGCAGAGGTT CCTGTCAGAA TATCCTCTG    | 180  |
| TCCAATGCAC CACTGGGCC TCAATTCCC TTCACAGGGG TGGATGACCG GGAGTCGTGG    | 240  |
| CCTTCCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT  | 300  |
| GGAAACTGCA AGTTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA  | 360  |
| AGAAACATCT TCGATTGAG TGCCCCAGAG AAGGACAAAT TTTTGCCCTA CCTCACTTTA   | 420  |
| GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA  | 480  |
| AATGGATCAA CACCATGTT TAACGACATC AATATTATG ACCTCTTGT CTGGATGCAT     | 540  |
| TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTT  | 600  |
| GCCCCATGAAG CACCAGCTTT TCTGCCTTGG CATAGACTCT TCTTGTGCG GTGGGAACAA  | 660  |
| GAAATCCAGA AGCTGACAGG AGATGAAAAC TTCACTATTC CATATTGGGA CTGGCGGGAT  | 720  |
| GCAGAAAAGT GTGACATTG CACAGATGAG TACATGGAG GTCAGCACCC CACAAATCCT    | 780  |
| AACTTACTCA GCCCAGCATE ATTCTTCTCC TCTTGGCAGA TTGTCTGTAG CCGATTGGAG  | 840  |
| GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCG AGGGACCTTT ACGGCGTAAT  | 900  |
| CCTGGAAACC ATGACAAATC CAGAACCCCA AGGCTCCCCT CTTCAGCTGA TGTAGAATTT  | 960  |
| TGCCTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT  | 1020 |
| AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGGA TAGCGGATGC CTCTCAAAGC  | 1080 |
| AGCATGCACA ATGCCTTGCA CATCTATATG AATGGAACAA TGTCCCAGGT ACAGGGATCT  | 1140 |
| GCCAACGATC CTATCTTCCCT TCTTCACCAT GCATTTGTTG ACAGTATTTT TGAGCAGTGG | 1200 |

|  |      |
|--|------|
| CTCCGAAGGC ACCGTCCCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT | 1260 |
| AACCGGGAAT CCTACATGGT TCCTTTATA CCACTGTACA GAAATGGTGA TTTCTTTATT   | 1320 |
| TCATCCAAAG ATCTGGCTA TGACTATAGC TATCTACAAG ATTCAAGACCC AGACTCTTT   | 1380 |
| CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GCTCCTTGGG  | 1440 |
| GCGGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT  | 1500 |
| CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT  | 1560 |
| TACCACAGCT TGTATCAGAG CCATTAA                                      | 1587 |

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

|   |      |
|---|------|
| ATGCTCCTGG CTGTTTGTA CTGCCTGCTG TGGAGTTCC AGACCTCCGC TGGCCATTTC   | 60   |
| CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC | 120  |
| GGGGACAGGA GTCCCTGTGG CCAGCTTCA GGCAGAGGTT CCTGTCAGAA TATCCTTCTG  | 180  |
| TCCAATGCAC CACTTGGCC TCAATTCCC TTCACAGGGG TGGATGACCG GGAGTCGTGG   | 240  |
| CCTTCCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT | 300  |
| GGAAACTGCA AGTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA  | 360  |
| AGAAAACATCT TCGATTGAG TGCCCCAGAG AAGGACAAAT TTTTGCCCTA CCTCACTTTA | 420  |
| GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA | 480  |
| AATGGATCAA CACCCATGTT TAACGACATC AATATTATG ACCTCTTGT CTGGATGCAT   | 540  |
| TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTC | 600  |
| GCCCATGAAG CACCAAGCTT TCTGCCTTGG CATAGACTCT TCTTGTGGCG GTGGGAACAA | 660  |
| GAAATCCAGA AGCTGACAGG AGATGAAAAT TTCACTATTC CATATTGGGA CTGGCGGGAT | 720  |
| GCAGAAAAGT GTGACATTTG CACAGATGAG TACATGGAG GTCAGCACCC CACAAATCCT  | 780  |
| AACTTACTCA GCCCAGCCTC ATTCTCTCC TCTTGGCAGA TTGCTGTAG CCGATTGGAG   | 840  |
| GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCG AGGGACCTTT ACGGCGTAAT | 900  |
| CCTGGAAACC ATGACAAATC CAGAACCCCA AGGCTCCCT CTTCAGCTGA TGTAGAATTT  | 960  |
| TGCCTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT | 1020 |
| AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGGA TAGCGGATGC CTCTCAAAGC | 1080 |

|   |      |
|---|------|
| AGCATGCACA ATGCCTTGCA CATCTATATG AATGGAACAA TGTCCCAGGT ACAGGGATCT | 1140 |
| GCCAACGATC CTATCTTCCT TCTTCACCAT GCATTTGTTG ACAGTATTT TGAGCAGTGG  | 1200 |
| CTCCGAAGGC ACCGTCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT  | 1260 |
| AACCAGGAAT CCTACATGGT TCCTTTTATA CCACTGTACA GAAATGGTGA TTTCTTTATT | 1320 |
| TCATCCAAAG ATCTGGGCTA TGACTATAGC TATCTACAAG ATTCAAGACCC AGACTCTTT | 1380 |
| CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GCTCCTTGGG | 1440 |
| GCAGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT | 1500 |
| CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT | 1560 |
| TACCAACAGCT TGTATCAGAG CCATTAA                                    | 1587 |

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TAAATGGCTC TGATACAAGC T 21

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCAAGTTTGG CTTTTGGGGA 20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGCTCCTGG CTGTTTGTA CTG 23

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

|  |     |
|--|-----|
| CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC  | 60  |
| CATTTCCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTG CCGGTTATGT CTAATGGGTG | 120 |
| CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG                           | 157 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

|  |     |
|--|-----|
| CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC  | 60  |
| CATTTCCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTG CTGGTTATGT CCAATGGGTG | 120 |
| CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG                           | 157 |

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

|                          |    |
|--------------------------|----|
| GGTTGGCCAA TCTACTCCCA GG | 22 |
|--------------------------|----|

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

|                       |    |
|-----------------------|----|
| GCTCACTCAG TGTGGCAAAG | 20 |
|-----------------------|----|

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|   |     |
|---|-----|
| GGTTGGCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC   | 60  |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT | 120 |
| CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG  | 300 |
| GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT | 360 |
| GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCCTTAG | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC     | 536 |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 534 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

|  |     |
|--|-----|
| GGTTGGCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC    | 60  |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT  | 120 |
| CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGGTCT GCCGTTACTG CCCTGTGGGG  | 180 |
| CAAGGTGAAC GTGGATGAAG TTGGTGGTGA GGCCCTGGC AGGTTGGTAT CAAGGTTACA   | 240 |
| AGACAGGTTT AAGGAGACCA ATAGAAAATG GGCATGTGGA GACAGAGAAG ACTCTTGGGT  | 300 |
| TTCTGATAGG CACTGACTCT CTCTGCCTAT TGGTCTATTT TCCCACCCCTT AGGCTGCTGG | 360 |
| TGGTCTACCC TTGGACCCAG AGGTCTTTG AGTCCTTTGG GGATCTGTCC ACTCCTGATG   | 420 |
| CTGTTATGGG CAACCCTAAG GTGAAGGCTC ATGGCAAGAA AGTGCTCGGT GCCTTTAGTG  | 480 |
| ATGGCCTGGC TCACCTGGAC AACCTCAAGG GCACCTTTGC CACACTGAGT GAGC        | 534 |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

|  |     |
|--|-----|
| GGTTGGCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC    | 60  |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGAACCT   | 120 |
| CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA  | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG  | 300 |
| GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT  | 360 |
| GGTGGTCTAC CCTTGGACCT AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA  | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTAG   | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC      | 536 |

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|  |     |
|--|-----|
| GGTTGGCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC    | 60  |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGAACCT   | 120 |
| CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGAGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA  | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG  | 300 |
| GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT  | 360 |
| GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA  | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTAG   | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC      | 536 |

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 64 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAAUACUCAA GCUUGCAUGC CUGCAGGUCG ACUCUAGAGG AUCCCCGGGU ACCGAGCUCG 60

AAUUU 64

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GGCTGACAAG AAGGAAACTC 20

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCAGGCGGCG GCTAGGAGAG ATGGG 25

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60

GAGGTACTGG GGAGGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC 120

ATTTCGCTCT GTATTCAAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTTC 180

TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240

CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300

ATTTTAGAAG TAGGCCAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G

351

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

|   |     |
|---|-----|
| GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG | 60  |
| GAGGAGCCGG TCGGGAACAC CCACCTTCTT GATGTATAAA TATCACTGCA TTTCGCTCTG | 120 |
| TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT | 180 |
| AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACCTAGCC AGTGCTGGC  | 240 |
| AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT | 300 |
| AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG                       | 340 |

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

|   |     |
|---|-----|
| GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG | 60  |
| GAGGAGCCGG TCGGGAACAC CCACCTTCTT GGTGTATAAA TATCACTGCA TTTCGCTCTG | 120 |
| TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT | 180 |
| AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACCTGGCC AGTGCTGGC  | 240 |
| AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT | 300 |
| AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG                       | 340 |

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60  
GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC 120  
ATTCGCTCT GTATTCAAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTTC 180  
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240  
CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300  
ATTTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGCTGACAAG AAGGAAACTC GCTGAAACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60  
GAGGTACTGG GAAGGAGCCG GTCGGGAACG CCCACTTTCT TGATGTATAA ATATCACTGC 120  
ATTCGCTCT GTATTCAAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTTC 180  
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240  
CGGTGCTGGG CAGAGTGAAT CCACGCTTGC TTGCTTAAAG CCCTCTTCAA TAAAGCTGCC 300  
ATTTTAGAAG TAAGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 351 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60  
GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC 120  
ATTCGCTCT GTATTCAAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TAGGAGGTTTC 180  
TCTCCAGCAC TAGCAGGTAG AGCCTGAGTG TTCCCTGCTA AACTCTCACC AGCACTTGGC 240  
CGGTGCTGGG CAGAGCGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300  
ATTTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

|   |     |
|---|-----|
| GGTTGGCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC   | 60  |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT | 120 |
| CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGTGGT AAGGCCCTGG GCAGGTTGGT ATCAAGGTTA | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG  | 300 |
| GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT | 360 |
| GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTAG  | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC     | 536 |

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 536 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

|   |     |
|---|-----|
| GGTTGGCAA TCTACTCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC   | 60  |
| AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT | 120 |
| CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG | 180 |
| GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA | 240 |
| CAAGACAGGT TTAAGGAGAC CAATAGAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG  | 300 |
| GTTTCTGATA GGCACTGACT CTCTCTGCCT ATTAGTCTAT TTTCCCACCC TTAGGCTGCT | 360 |
| GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA | 420 |
| TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTAG  | 480 |
| TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC     | 536 |

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 157 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

|   |     |
|---|-----|
| CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA | 60  |
| TCCTACATGG TTCCTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA  | 120 |
| GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAAG                         | 157 |

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

|   |     |     |     |
|---|-----|-----|-----|
| Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu |     |     |     |
| 1   | 5   | 10  | 15  |
| Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys |     |     |     |
| 20  | 25  | 30  |     |
| Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe |     |     |     |
| 35  | 40  | 45  |     |
| Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile |     |     |     |
| 50  | 55  | 60  |     |
| Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly |     |     |     |
| 65  | 70  | 75  | 80  |
| Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln |     |     |     |
| 85  | 90  | 95  |     |
| Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu |     |     |     |
| 100   | 105 | 110 |     |
| Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys |     |     |     |
| 115   | 120 | 125 |     |
| Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys |     |     |     |
| 130   | 135 | 140 |     |
| Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu |     |     |     |
| 145   | 150 | 155 | 160 |
| Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg |     |     |     |
| 165   | 170 | 175 |     |
| Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp |     |     |     |
| 180   | 185 | 190 |     |

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525

Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
530 535 540

Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
565 570 575

Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
580 585 590

Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
595 600 605

Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
610 615 620

Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
625 630 635 640

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
675 680 685

Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
690 695 700

Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
705 710 715 720

Val Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala  
725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750

Pro Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 548 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Ala Cys Lys Leu Gly Thr Gly Arg Arg  
 530 535 540  
 Phe Thr Thr Ser  
 545

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 695 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

DRAFT

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285

Leu Glu Ser Pro Lys Ala Leu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300

Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
305 310 315 320

Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala  
325 330 335

Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Trp Gly Arg Leu Glu Gly Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ser His Pro Leu  
675 680 685

Arg Gly Gly Pro Gly Leu His  
690 695

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 310 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240

Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro  
 290 295 300  
 Trp Arg Trp Arg Trp Gly  
 305 310

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 322 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Ala Ser Met Thr Gly Gly Gln Met Gly Arg Ile Asn Ser Gly  
 1 5 10 15  
 Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
 20 25 30  
 His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr  
 35 40 45  
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
 50 55 60  
 Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp  
 65 70 75 80  
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Tyr Lys Ala  
 85 90 95  
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
 100 105 110  
 Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly  
 115 120 125  
 Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys  
 130 135 140  
 Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln  
 145 150 155 160  
 Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile  
 165 170 175  
 Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp  
 180 185 190

Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly  
195 200 205

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp  
210 215 220

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala  
225 230 235 240

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp  
245 250 255

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala  
260 265 270

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg  
275 280 285

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro  
290 295 300

Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro Trp Arg Trp Arg  
305 310 315 320

**Trp Gly**

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 528 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
1 5 10 15

His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr  
20 25 30

Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
35 40 45

Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp  
50 55 60

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala  
65 70 75 80

Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
85 90 95

Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly  
100 105 110

Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys  
115 120 125

Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln  
130 135 140

Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile  
145 150 155 160

Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp  
165 170 175

Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly  
180 185 190

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp  
195 200 205

Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala  
210 215 220

Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp  
225 230 235 240

Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala  
245 250 255

Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg  
260 265 270

Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro  
275 280 285

Lys Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala  
290 295 300

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
305 310 315 320

Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr  
325 330 335

Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro  
340 345 350

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
355 360 365

Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
370 375 380

Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
385 390 395 400

Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val  
405 410 415

Glu Thr Leu Phe Gly Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg  
420 425 430

Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
435 440 445

Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
450 455 460

Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His  
465 470 475 480

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala  
485 490 495

Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro  
500 505 510

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
515 520 525

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 315 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Ala Ser Met Thr Gly Gly Gln Met Gly Arg Ile Asn Ser Gly  
1 5 10 15

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly  
20 25 30

His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr  
35 40 45

Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu  
50 55 60

Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp  
65 70 75 80

Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Tyr Lys Ala  
85 90 95

Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile  
100 105 110

Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly  
115 120 125

Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys  
130 135 140

Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln  
145 150 155 160

Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile  
165 170 175

Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp  
180 185 190

Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly  
195 200 205

Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp  
 210 215 220  
 Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala  
 225 230 235 240  
 Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp  
 245 250 255  
 Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala  
 260 265 270  
 Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg  
 275 280 285  
 Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro  
 290 295 300  
 Lys Ala Ala Leu Glu His His His His His His  
 305 310 315

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

|  |     |
|--|-----|
| ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTCA   | 60  |
| GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG  | 120 |
| GATGATTGTA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA  | 180 |
| GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCGGTGG CCCCTGCACC AGCAGCTCCT   | 240 |
| ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCTGT CATCTTCTGT CCCTTCCCAG   | 300 |
| AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG  | 360 |
| TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAAGATGT TTTGCCAACT GGCCAAGACC | 420 |
| TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCG GCACCCGCGT CCGCGCCATG   | 480 |
| GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCGCTGCC CCACCATGAG   | 540 |
| CGCTGCTCAG ATAGCGATGG TCTGGCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT   | 600 |
| TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT  | 660 |
| GAGCCGCCTG AGGTTGGCTC TGACTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT  | 720 |
| TCCTGCATGG GCGGCATGAA CCGGAGGCC ATCCTCACCA TCATCACACT GGAAGACTCC   | 780 |
| AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA  | 840 |
| GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCC   | 900 |

|  |      |
|--|------|
| CCAGGGAGCA CTAAGCGAGC ACTGCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG   | 960  |
| AAACCACTGG ATGGAGAATA TTTCACCCCTT CAGATCCGTG GGCGTGAGCG CTTCGAGATG | 1020 |
| TTCCGAGAGC TGAATGAGGC CTTGGAACTC AAGGATGCC AGGCTGGAA GGAGCCAGGG    | 1080 |
| GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAGG GTCAGTCTAC CTCCCGCCAT   | 1140 |
| AAAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA                     | 1182 |

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

|  |      |
|--|------|
| ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTCA   | 60   |
| GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG  | 120  |
| GATGATTGAGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA | 180  |
| GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCGTGG CCCCTGCACC AGCAGCTCCT    | 240  |
| ACACCGGCCG AGCCCTGCACC AGCCCCCTCC TGGCCCTGT CATCTTCTGT CCCTTCCCAG  | 300  |
| AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG  | 360  |
| TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAAGATGT TTTGCCAACT GGCCAAGACC | 420  |
| TGCCCTGCGC AGCTGTGGGT TGATTCCACA CCCCGCCCG GCACCCGCGT CCGGCCATG    | 480  |
| GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCGCTGCC CCACCATGAG   | 540  |
| CGCTGCTCAG ATAGCGATGG TCTGGCCCT CCTCAGCATH TTATCCGAGT GGAAGGAAAT   | 600  |
| TTGCGTGTGG AGTATTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT   | 660  |
| GAGCCGCTG AGGTTGGCTC TGACTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT   | 720  |
| TCCTGCATGG GCGGCATGAA CCGGAGGCC ACCCTCACCA TCATCACACT GGAAGACTCC   | 780  |
| AGTGGTAATC TACTGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCCTG TCCTGGGAGA  | 840  |
| GACCGGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCC  | 900  |
| CCAGGGAGCA CTAAGCGAGC ACTGCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG   | 960  |
| AAACCACTGG ATGGAGAATA TTTCACCCCTT CAGATCCGTG GGCGTGAGCG CTTCGAGATG | 1020 |
| TTCCGAGAGC TGAATGAGGC CTTGGAACTC AAGGATGCC AGGCTGGAA GGAGCCAGGG    | 1080 |
| GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAGG GTCAGTCTAC CTCCCGCCAT   | 1140 |
| AAAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA                     | 1182 |

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

|   |      |
|---|------|
| ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTCA    | 60   |
| GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG   | 120  |
| GATGATTGTA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA   | 180  |
| GATGAAGCTC CCAGAACATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT | 240  |
| ACACCGGCCGG CCCCTGCACC AGCCCCCTCC TGGCCCCCTGT CATCTTCTGT CCCCTCCAG  | 300  |
| AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCAATTCTGG GACAGCCAAG  | 360  |
| TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAAGATGT TTTGCCAACT GGCAAGACC   | 420  |
| TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCCG GCACCCCGCGT CCGCGCCATG  | 480  |
| GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCCTGCCCC CCACCATGAG   | 540  |
| CGCTGCTCAG ATAGCGATGG TCTGGCCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT  | 600  |
| TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT   | 660  |
| GAGCCGCCTG AGGTTGGCTC TGACTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT   | 720  |
| TCCTGCATGG GCGGCATGAA CCGGAGACCC ATCCTCACCA TCATCACACT GGAAGACTCC   | 780  |
| AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCCTG TCCTGGGAGA  | 840  |
| GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCC    | 900  |
| CCAGGGAGCA CTAAGCGAGC ACTGCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG    | 960  |
| AAACCACCTGG ATGGAGAATA TTTCACCCCTT CAGATCCGTG GGCCTGAGCG CTTCGAGATG | 1020 |
| TTCCGAGAGC TGAATGAGGC CTTGGAACTC AAGGATGCC AGGCTGGGAA GGAGCCAGGG    | 1080 |
| GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAGG GTCAGTCTAC CTCCCGCCAT    | 1140 |
| AAAAAACTCA TGTTCAAGAC AGAAGGGCCT GACTCAGACT GA                      | 1182 |

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCTGGGCTTC TTGCATTCTG

20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGGGCAGT GCTCGCTTAG

20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

|  |     |
|--|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT   | 60  |
| CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC  | 120 |
| ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC  | 180 |
| GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC  | 240 |
| TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTGG ATGACAGAAA   | 300 |
| CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC  | 360 |
| CACCATCCAC TACAAC TACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC | 420 |
| CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT  | 480 |
| TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG  | 540 |
| CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCAA   | 600 |
| C  | 601 |

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT 60  
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC 120  
AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT 180  
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT 240  
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT 300  
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG 360  
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAAACCTC 420  
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCG ACGCGGGTGC CGGGCGGGGG 480  
TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGAAA ACATCTTGT 540  
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG 600  
**A** 601

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCTGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT 60  
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGCG CAGCTGTGGG TTGATTCCAC 120  
ACCCCCGCCC GGCACCCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC 180  
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC 240  
TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTGGG ATGACAGAAA 300  
CACTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC 360  
CACCACATCCAC TACAACATACA TGTGTAACAG TTCCTGCATG GGCAGGCGATGA ACCGGAGGCC 420  
CATCCTCACC ATCATCACAC TGGAAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT 480  
TGAGGTGCGT GTTTGTGCCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG 540  
CAAGAAAGGG GAGCCTCACCA CCGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA 600  
**C** 601

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

|   |     |
|---|-----|
| GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTCCTT | 60  |
| CGGGAGATTG TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC | 120 |
| AAAGCTGTTG CGTCCCAGTA GATTACACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT  | 180 |
| GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT | 240 |
| GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT | 300 |
| GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCCTCC ACTCGGATAA GATGCTGAGG | 360 |
| AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC | 420 |
| CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACCGGGGTGC CGGGCGGGGG | 480 |
| TGTGGAATCA ACCCACAGCT GCGCAGGGCA GGTCTTGGCC AGTTGGCAA ACATCTTGTT  | 540 |
| GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG | 600 |
| A   | 601 |

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

|  |     |
|--|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT  | 60  |
| CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC  | 120 |
| ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC  | 180 |
| GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC  | 240 |
| TCCTCAGCAT CTTATCCGAG TGGAGGAAA TTTGCGTGTG GAGTATTGAG ATGACAGAAA   | 300 |
| CACTTTTCGA CATACTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC  | 360 |
| CACCATCCAC TACAACCTACA TGTGTAACAG TTCTGCATG GCGGCATGA ACCGGAGACC   | 420 |
| CATCCTCACC ATCATCACAC TGGAAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT | 480 |
| TGAGGTGCGT GTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG   | 540 |
| CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA  | 600 |

## (2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

|   |     |
|---|-----|
| GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT   | 60  |
| GCGGAGATTC TCTTCCTCTG TCGGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC   | 120 |
| AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT   | 180 |
| GGGTCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT   | 240 |
| GGTACAGTCA GAGCCAACCT CAGGCAGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT  | 300 |
| GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCTTCC ACTCGGATAA GATGCTGAGG   | 360 |
| AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC   | 420 |
| CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGCG CGGGCGGGGG  | 480 |
| TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGT    | 540 |
| GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAACATGCA AGAACGCCAG | 600 |
| A   | 601 |

## (2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

|                          |    |
|--------------------------|----|
| GAGGATGGGA CTCCGGTTCA TG | 22 |
|--------------------------|----|

## (2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CATGAACCGG AGTCCCATCC TCAC

24

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCACAAACAT GCACCTCAAA GCT

23

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGCTTGAG GTGCATGTTT GT

22

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 601 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

|  |     |
|--|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT  | 60  |
| CAACAAGATG TTTTGCCAAC TG GCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC | 120 |
| ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC  | 180 |
| GGAGGTTGTG AGGCCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC   | 240 |
| TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTGG ATGACAGAAA  | 300 |
| CACTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC   | 360 |
| CACCATCCAC TACAAC TACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGTCC | 420 |
| CATCCTCACC ATCATCACAC TGGAAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT | 480 |
| TGAGGTGCGT GTTGTGCCT GTCCTGGGAG AGACCGGGCGC ACAGAGGAAG AGAATCTCCG  | 540 |
| CAAGAAAGGG GAGCCTCAC CACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA  | 600 |

## (2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 601 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

|   |     |
|---|-----|
| GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT     | 60  |
| GCGGAGATTG TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC     | 120 |
| AAAGCTGTTG CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT     | 180 |
| GGGACTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT     | 240 |
| GGTACAGTCA GAGCCAACCT CAGGGGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT     | 300 |
| GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCCTTCC ACTCGGATAA GATGCTGAGG    | 360 |
| AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC     | 420 |
| CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACCGGGGTGC CGGGCGGGGG     | 480 |
| TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGAAA ACATCTTGT       | 540 |
| GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAACATGCA AGAACAGCCCAG | 600 |
| A   | 601 |

## (2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 601 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

|   |     |
|---|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT   | 60  |
| CAACAAGATG TTTTGCCAAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC  | 120 |
| ACCCCCGCCCG GGCACCCCGCG TCCCGGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC | 180 |
| GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC   | 240 |
| TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTGAG ATGACAGAAA  | 300 |
| CACTTTTCGA CATACTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC   | 360 |
| CACCATCCAC TACAACATACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC  | 420 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| CATCCTCAC  | ATCATCACAC | TGGAAGACTC | CAGTGGTAAT | CTACTGGGAC | GGAACAGCTT | 480 |
| TGAGGTGCAT | TTTGTCGCCT | GTCCTGGAG  | AGACCGGC   | ACAGAGGAAG | AGAATCTCCG | 540 |
| CAAGAAAGGG | GAGCCTCAC  | ACGAGCTGCC | CCCAGGGAGC | ACTAAGCGAG | CACTGCCAA  | 600 |
| C          |            |            |            |            |            | 601 |

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

|            |                     |                     |                     |                     |                     |     |
|------------|---------------------|---------------------|---------------------|---------------------|---------------------|-----|
| GTTGGGCAGT | GCTCGCTTAG          | TGCTCCCTGG          | GGGCAGCTCG          | TGGTGAGGCT          | CCCCTTCIT           | 60  |
| GCGGAGATT  | C T T C C T C T G   | T G C G C C G G T C | T C T C C A G G A   | C A G G C A C A A A | C A T G C A C C T C | 120 |
| AAAGCTGTT  | C G T C C C A G T A | G A T T A C C A T   | G G A G T C T T C C | A G T G T G A T G A | T G G T G A G G A T | 180 |
| GGGCCTCCGG | T T C A T G C C G C | C C A T G C A G G A | A C T G T T A C A C | A T G T A G T T G T | A G T G G A T G G T | 240 |
| GGTACAGTCA | G A G C C A A C C T | C A G G C G G C T C | A T A G G G C A C C | A C C A C A C T A T | G T C G A A A A G T | 300 |
| GTTTCTGTCA | T C C A A A T A C T | C C A C A C G C A A | A T T T C C T T C C | A C T C G G A T A A | G A T G C T G A G G | 360 |
| AGGGGCCAGA | C C A T C G C T A T | C T G A G C A G C G | C T C A T G G T G G | G G G C A G C G C C | T C A C A A C C T C | 420 |
| CGTCATGTGC | T G T G A C T G C T | T G T A G A T G G C | C A T G G C G C G G | A C G C G G G T G C | C G G G C G G G G G | 480 |
| TGTGGAATCA | A C C C A C A G C T | G C A C A G G G C A | G G T C T T G G C C | A G T T G G C A A A | A C A T C T T G T T | 540 |
| GAGGGCAGGG | G A G T A C G T G C | A A G T C A C A G A | C T T G G C T G T C | C C A G A A T G C A | A G A A G C C C A G | 600 |
| A          |                     |                     |                     |                     |                     | 601 |

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 427 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

|                     |                     |                     |                     |                     |                     |     |
|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|-----|
| TCTGGGCTTC          | T T G C A T T C T G | GGACAGCAA           | G T C T G T G A C T | T G C A C G T A C T | C C C T G C C C T   | 60  |
| CAACAAGATG          | T T T T G C C A A C | T G G C C A A G A C | C T G C C C T G T G | C A G C T G T G G G | T T G A T T C C A C | 120 |
| A C C C C C G C C C | G G C A C C C G C G | T C C G C G C C A T | G G C C A T C T A C | A A G C A G T C A C | A G C A C A T G A C | 180 |
| GGAGGTTGTG          | A G G C G C T G C C | C C C A C C A T G A | G C G C T G C T C A | G A T A G C G A T G | G T C T G G C C C C | 240 |

|  |     |
|--|-----|
| TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTGG ATGACAGAAA  | 300 |
| CACTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC   | 360 |
| CACCATCCAC TACAACATACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGTCC | 420 |
| CATCCTC  | 427 |

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 196 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

|   |     |
|---|-----|
| CATGAACCGG AGTCCCATCC TCACCACATCACACACTGGAA GACTCCAGTG GTAATCTACT | 60  |
| GGGACGGAAC AGCTTTGAGG TGCCTGTTTG TGCCCTGCCT GGGAGAGACC GGCGCACAGA | 120 |
| GGAAGAGAAT CTCCGCAAGA AAGGGGAGCC TCACCACGAG CTGCCCCCAG GGAGCACTAA | 180 |
| GCGAGCACTG CCCAAC   | 196 |

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 498 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

|   |     |
|---|-----|
| TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGACAGTACT CCCCTGCCCT   | 60  |
| CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC   | 120 |
| ACCCCCGCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC    | 180 |
| GGAGGTTGTG AGGCCTGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC | 240 |
| TCCTCAGCAT CTTATCCGAG TGGAAAGGAAA TTTGCGTGTG GAGTATTGG ATGACAGAAA   | 300 |
| CACTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC    | 360 |
| CACCATCCAC TACAACATACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC  | 420 |
| CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGAC GGAACAGCTT    | 480 |
| TGAGGTGCAT GTTTGTGC   | 498 |

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 127 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

|  |     |
|--|-----|
| CAGCTTGAG GTGCATGTTT GTGCCGTGCC TGGGAGAGAC CGGCGCACAG AGGAAGAGAA | 60  |
| TCTCCGCAAG AAAGGGGAGC CTCACCACGA GCTGCCCCA GGGAGCACTA AGCGAGCACT | 120 |
| GCCCCAAC   | 127 |

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

|                      |    |
|----------------------|----|
| GGTTTTCTT TGAGGTTTAG | 20 |
|----------------------|----|

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

|                      |    |
|----------------------|----|
| GCGACACTCC ACCATAGAT | 19 |
|----------------------|----|

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

|                      |    |
|----------------------|----|
| CTGTCTTCAC GCAGAAAGC | 19 |
|----------------------|----|

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

D  
D  
D  
D  
D  
D  
D  
D  
D  
D  
D  
D  
D  
D

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCACGGTCTA CGAGACCTC

19

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GATCTACTAG TCATATGGAT

20

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TCGGTACCCG GGGATCCGAT

20

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 281 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCTGT CAGCCTCCAG

60

GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGAACCC GGTGAGTACA CCGGAATTGC

120

CAGGACGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC

180

CCCGCAAGAC TGCTAGCCGA GTAGTGTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT

240

AGGGTGCCTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C

281

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 386 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

|   |     |
|---|-----|
| CTGTCTTCAC GCAGAAAGCG TCTGCCATG GCGTTAGTAT GAGTGTCTGT CAGCCTCCAG  | 60  |
| GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGACTGTC TTCACGCAGA | 120 |
| AAGCGTCTAG CCATGGCGTT AGTATGAGTG TCGTGCAGCC TCCAGGACCC CCCCTCCGG  | 180 |
| GAGAGCCATA GTGGTCTGCG GAACCGGTGA GTACACCGGA ATTGCCAGGA CGACCGGGTC | 240 |
| CTTTCTTGA TCAACCCGCT CAATGCCTGG AGATTGGC GTGCCCGCG AAGACTGCTA     | 300 |
| GCCGAGTAGT GTTGGGTCGC GAAAGGCCTT GTGGTACTGC CTGATAGGGT GCTTGCGAGT | 360 |
| GCCCCGGGAG GTCTCGTAGA CCGTGC                                      | 386 |

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 281 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

|  |     |
|--|-----|
| CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGT CAGCCTCCAG  | 60  |
| GTCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC | 120 |
| CAGGACGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC  | 180 |
| CCCGCGAGAC TGCTAGCCGA GTAGTGTGG GTCGCAAAG GCCTTGTGGT ACTGCCTGAT    | 240 |
| AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C                      | 281 |

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

|   |     |
|---|-----|
| CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCTGT CAGCCTCCAG | 60  |
| GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC | 120 |
| CAGGACGACC GGGTCCTTTC GTGGATGTAA CCCGCTCAAT GCCTGGAGAT TTGGGCGTG  | 180 |

|   |     |
|---|-----|
| CCCCGCAAGA CTGCTAGCCG AGTAGTGTG GGTGCGAAA GGCTTGTT TACTGCCTGA | 240 |
| TAGGGTGCTT GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GC                | 282 |

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

|   |     |
|---|-----|
| CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAC GAGTGTGTA CAGCCTCCAG    | 60  |
| GCCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGAACCC GGTGAGTACA CCGGAATTGC  | 120 |
| CGGAAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG CCCGGCCATT TGGGCGTGCC   | 180 |
| CCCGCAAGAC TGCTAGCCGA GTAGCGTTGG GTTGCAGAAAG GCCTTGTTGGT ACTGCCTGAT | 240 |
| AGGGTGCTTG CGAGTACCCCC GGGAGGTCTC GTAGACCGTG C                      | 281 |

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

|  |     |
|--|-----|
| CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAC GAGTGTGTA CAGCCTCCAG     | 60  |
| GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGAACCC GGTGAGTACA CCGGAATCGC    | 120 |
| TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA CCCAGAAATT TGGGCGTGCC    | 180 |
| CCCGCGAGAT CACTAGCCGA GTAGTGTGTTGG GTAGCGAAAG GCCTTGTTGGT ACTGCCTGAT | 240 |
| AGGGTGCTTG CGAGTACCCCC GGGAGGTCTC GTAGACCGTG C                       | 281 |

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

|  |    |
|--|----|
| GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAGGCACCC TATCAGGCAG TACCACAGG | 60 |
|--|----|

|   |     |
|---|-----|
| CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTGCGG GGGCACGCC AAATCTCCAG   | 120 |
| GCATTGAGCG GGTTTATCCA AGAAAGGACC CGGTCGTCTT GGCAATTCCG GTGTACTCAC | 180 |
| CGGTTCCGCA GACCACTATG GCTCTCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT  | 240 |
| CATACTAACG CCATGGCCAG ACGCTTCTG CGTGAAGACA G                      | 281 |

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 281 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

|  |     |
|--|-----|
| GCACGGTCTA CGAGACCTCC CGGGGCACCTC GCAAGCACCC TATCAGGCAG TACCACAAGG | 60  |
| CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTGCGG GGGCACGCC AAATCTCCAG    | 120 |
| GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCTT GGCAATTCCG GTGTACTCAC  | 180 |
| CGGTTCCGCA GACCACTATG GCTCTCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT   | 240 |
| CATACTAACG CCATGGCTAG ACGCTTCTG CGTGAAGACA G                       | 281 |

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 281 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

|  |     |
|--|-----|
| GCACGGTCTA CGAGACCTCC CGGGGCACCTC GCAAGCACCC TATCAGGCAG TACCACAAGG | 60  |
| CCTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTGCGG GGGCACGCC AAATCTCCAG    | 120 |
| GCATTGAGCG GGTTGATCCA AGAAAGGACC CGGTCGTCTT GGCAATTCCG GTGTACTCAC  | 180 |
| CGGTTCCGCA GACCACTATG GCTCTCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT   | 240 |
| CATACTAACG CCATGGCTAG ACGCTTCTG CGTGAAGACA G                       | 281 |

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 282 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

|   |     |
|---|-----|
| GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG | 60  |
| CCTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCAG GGGCACGCC AAATCTCCAG   | 120 |
| GCATTGAGCG GGTTACATCC ACGAAAGGAC CCGGTCGTCC TGGCAATTCC GGTGTACTCA | 180 |
| CCGGTTCCGC AGACCACTAT GGCTCTCCCG GGAGGGGGGG TCCTGGAGGC TGCACGACAC | 240 |
| TCATACTAAC GCCATGGCTA GACGCTTCT GC GTGAAGAC AG                    | 282 |

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

|   |     |
|---|-----|
| GCACGGTCTA CGAGACCTCC CGGGGTACTC GCAAGCACCC TATCAGGCAG TACCACAAGG | 60  |
| CCTTCGCAA CCCAACGCTA CTCGGCTAGC AGTCTTGCAG GGGCACGCC AAATGGCCGG   | 120 |
| GCATAGAGTG GGTTTATCCA AGAAAGGACC CAGTCTCCCC GGCAATTCCG GTGTACTCAC | 180 |
| CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGG CCTGGAGGCT GTACGACACT  | 240 |
| CATACTAACG CCATGGCTAG AC GCTTCTG CGTGAAGACA G                     | 281 |

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

|   |     |
|---|-----|
| GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG | 60  |
| CCTTCGCGA CCCAACACTA CTCGGCTAGT GATCTCGCGG GGGCACGCC AAATTCTGG    | 120 |
| GTATTGAGCG GGTTGCTCCA AGAAAGGACC CGGTCAACCC AGCGATTCCG GTGTACTCAC | 180 |
| CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGT CCTGGAGGCT GCACGACACT  | 240 |
| CGTACTAACG CCATGGCTAG GCGCTTCTG CGTGAAGACA G                      | 281 |

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ATCAACATCC GGCCGGTGGT

20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGGGCCTCGC TACGGACCAG

20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

|   |     |
|---|-----|
| ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC   | 60  |
| CAATTCACTGG ACCAGAACAA CCCGCTGTCTG GGGTTGACCC ACAAGCGCCG ACTGTCGGCG | 120 |
| CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG   | 180 |
| TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC   | 240 |
| GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTGGGT TCATCGAAAC GCCGTACCGC    | 300 |
| AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC   | 360 |
| CGCCACGTGG TGGCACAGGC CAATTGCGCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG   | 420 |
| CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC   | 480 |
| TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG   | 540 |
| GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG   | 600 |
| CTGGTCCGTA GCGAGGCCCC   | 620 |

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

|  |     |
|--|-----|
| ATCAACATCC GGCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC   | 60  |
| CAATTCAATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCT ACAAGCGCCG ACTGTGGCG  | 120 |
| CTGGGGCCCG GCGGTCTGTC ACAGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG | 180 |
| TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC  | 240 |
| GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTGGGT TCATCGAAAC GCCGTACCGC   | 300 |
| AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC  | 360 |
| CGCCACGTGG TGGCACAGGC CAATTGCGCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG  | 420 |
| CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC  | 480 |
| TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG  | 540 |
| GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG  | 600 |
| CTGGTCCGTA GCGAGGCCCC  | 620 |

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

|  |     |
|--|-----|
| ATCAACATCC GGCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC   | 60  |
| CAATTCAATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGCGCCG ACTGTGGCG  | 120 |
| CTGGGGCCCG GCGGTCTGTC ACAGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG | 180 |
| TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC  | 240 |
| GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTGGGT TCATCGAAAC GCCGTACCGC   | 300 |
| AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC  | 360 |
| CGCCACGTGG TGGCACAGGC CAATTGCGCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG  | 420 |
| CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC  | 480 |
| TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG  | 540 |
| GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG  | 600 |
| CTGGTCCGTA GCGAGGCCCC  | 620 |

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

|   |     |
|---|-----|
| GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA | 60  |
| CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCG TGGCCACCGA CACCATCTGG  | 120 |
| CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCGCC  | 180 |
| TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG | 240 |
| GCCTGTGCCA CCACGTGGCG GTCCCTCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA | 300 |
| ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC | 360 |
| GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTGATCGGG  | 420 |
| CACATCCGGC CGTAGTGCAG CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT | 480 |
| GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG | 540 |
| TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGCG  | 600 |
| ACCACCGGCC GGATGTTGAT   | 620 |

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

|   |     |
|---|-----|
| GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA | 60  |
| CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCG TGGCCACCGA CACCATCTGG  | 120 |
| CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCGCC  | 180 |
| TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG | 240 |
| GCCTGTGCCA CCACGTGGCG GTCCCTCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA | 300 |
| ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC | 360 |
| GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTGATCGGG  | 420 |
| CACATCCGGC CGTAGTGCAG CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT | 480 |

GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCCTTGT AGGTCAACCC CGACAGCGGG 540  
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGCG 600  
ACCACCGGCC GGATGTTGAT 620

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 620 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GGGGCCTCGC TACGGACCAAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA 60  
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCCGG TG GCC ACCGAATTG 120  
CGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCGCC 180  
TTGGGGCGGA CCAGCACCGC CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG 240  
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA 300  
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC 360  
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG 420  
CACATCCGGC CGTAGTGCAGA CGGGTGCACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT 480  
GACAGACCGC CGGGCCCCAG CGCCAACAGT CGGCCTTGT GGGTCAACCC CGACAGCGGG 540  
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGCG 600  
ACCACCGGCC GGATGTTGAT 620

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AGCTCGTATG GCACCGGAAC 20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGACCTCCC ACCCGACTTG

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

|  |     |
|--|-----|
| AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG  | 60  |
| ACGAACACCC CGACGAAATG GGACAACAGT TTCCCTCGAGA TCCTGTACGG CTACGAGTGG | 120 |
| GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC  | 180 |
| GGCACCATCC CGGACCCGTT CGGGGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC  | 240 |
| CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTGCGCTGGCT GGAACACCCC | 300 |
| GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT  | 360 |
| CCCGTTGCGA GATACTTGG GCCGCTGGTC CCCAACGAGA CCCTGCTGTG GCAGGATCCG   | 420 |
| GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG  | 480 |
| ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTCGA CCGCATGGC GGCGGCGTCG    | 540 |
| TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTGCGATCCG CCTGCAGCCA  | 600 |
| CAAGTCGGGT GGGAGGTCAA  | 620 |

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

|  |     |
|--|-----|
| AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG  | 60  |
| ACGAACACCC CGACGAAATG GGACAACAGT TTCCCTCGAGA TCCTGTACGG CTACGAGTGG | 120 |
| GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC  | 180 |
| GGCACCATCC CGGACCCGTT CGGGGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC  | 240 |
| CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTGCGCTGGCT GGAACACCCC | 300 |

|   |     |
|---|-----|
| GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT | 360 |
| CCCGTTGCGA GATACTTGG GCCGCTGGTC CCCAACAGA CCCTGCTGTG GCAGGATCCG   | 420 |
| GTCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG  | 480 |
| ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTCGA CCGCATGGC GGCGGCGTCG   | 540 |
| TCGTTCCGTG GTAGCGACAA GCGCGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA  | 600 |
| CAAGTCGGGT GGGAGGTCAA   | 620 |

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

|   |     |
|---|-----|
| AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CGGGCATCGA GGTCGTATGG | 60  |
| ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG | 120 |
| GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC | 180 |
| GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC | 240 |
| CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTGCGTGGCT GGAACACCCC | 300 |
| GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT | 360 |
| CCCGTTGCGA GATACTTGG GCCGCTGGTC CCCAACAGA CCCTGCTGTG GCAGGATCCG   | 420 |
| GTCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG  | 480 |
| ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTCGA CCGCATGGC GGCGGCGTCG   | 540 |
| TCGTTCCGTG GTAGCGACAA GCGCGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA  | 600 |
| CAAGTCGGGT GGGAGGTCAA   | 620 |

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

|   |     |
|---|-----|
| AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CGGGCATCGA GGTCGTATGG | 60  |
| ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG | 120 |

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GAGCTGACGA | AGAGCCCTGC | TGGCGCTTGG | CAATACACCG | CCAAGGACGG | CGCCGGTGCC | 180 |
| GGCACCATCC | CGGACCCGTT | CGGCAGGCCA | GGGCCTCCC  | CGACGATGCT | GGCCACTGAC | 240 |
| CTCTCGCTGC | GGGTGGATCC | GATCTATGAG | CGGATCACGC | GTCGCTGGCT | GGAACACCCC | 300 |
| GAGGAATTGG | CCGACGAGTT | CGCCAAGGCC | TGGTACAAGC | TGATCCACCG | AGACATGGT  | 360 |
| CCCGTTGCGA | GATACCTTGG | GCCGCTGGTC | CCCAAGCAGA | CCCTGCTGTG | GCAGGATCCG | 420 |
| GTCCCTGCGG | TCAGCCACGA | CCTCGTCGGC | GAAGCCGAGA | TTGCCAGCCT | TAAGAGCCAG | 480 |
| ATCCTGGCAT | CGGGATTGAC | TGTCTCACAG | CTAGTTCGA  | CCGCATGGC  | GGCGGCGTCG | 540 |
| TCGTTCCGTG | GTAGCGACAA | GCGCGGCGGC | GCCAACGGTG | GTCGCATCCG | CCTGCAGCCA | 600 |
| CAAGTCGGGT | GGGAGGTCAA |            |            |            |            | 620 |

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

|            |            |             |            |            |            |     |
|------------|------------|-------------|------------|------------|------------|-----|
| TTGACCTCCC | ACCCGACTTG | TGGCTGCAGG  | CGGATGCGAC | CACCGTTGGC | GCCGCCGCGC | 60  |
| TTGTCGCTAC | CACGGAACGA | CGACGCCGCC  | GCCCATGCGG | TCGAAACTAG | CTGTGAGACA | 120 |
| GTCAATCCCG | ATGCCCCGAT | CTGGCTCTTA  | AGGCTGGCAA | TCTCGGCTTC | GCCGACGAGG | 180 |
| TCGTGGCTGA | CCGCAGGGAC | CGGATCCTGC  | CACAGCAGGG | TCTGCTTGGG | GACCAGCGGC | 240 |
| CCAAGGTATC | TCGCAACGGG | ACCCATGTCT  | CGGTGGATCA | GCTTGTACCA | GGCCTTGGCG | 300 |
| AACTCGTCGG | CCAATTCTC  | GGGGTGTTC   | AGCCAGCGAC | GCGTGATCCG | CTCATAGATC | 360 |
| GGATCCACCC | GCAGCGAGAG | GTCAGTGGCC  | AGCATCGTCG | GGGAGCGCCC | TGGCCCGCCG | 420 |
| AACGGGTCCG | GGATGGTGCC | GGCACCGGCCG | CCGTCCCTGG | CGGTGTATTG | CCAAGCGCCA | 480 |
| GCAGGGCTCT | TCGTCAGCTC | CCACTCGTAG  | CCGTACAGGA | TCTCGAGGAA | ACTGTTGTCC | 540 |
| CATITCGTCG | GGGTGTTCGT | CCATACGACC  | TCGATGCCGC | TGGTGATCGC | GTCCTTACCG | 600 |
| GTTCCGGTGC | CATAcgagct |             |            |            |            | 620 |

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

|   |     |
|---|-----|
| TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC | 60  |
| TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA | 120 |
| GTCAATCCCG ATGCCCGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG | 180 |
| TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGC  | 240 |
| CCAAGGTATC TCGAACCGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCTTGGCG  | 300 |
| AACTCGTCGG CCAATTCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC  | 360 |
| GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCC  | 420 |
| AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA | 480 |
| GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC | 540 |
| CATTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGG TGGTGATCGC GTCCTTACCG  | 600 |
| GTTCCGGTGC CATACTGAGCT  | 620 |

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

|   |     |
|---|-----|
| TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC | 60  |
| TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA | 120 |
| GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG | 180 |
| TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGC  | 240 |
| CCAAGGTATC TCGAACCGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCTTGGCG  | 300 |
| AACTCGTCGG CCAATTCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC  | 360 |
| GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCC  | 420 |
| AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA | 480 |
| GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC | 540 |
| CATTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG  | 600 |
| GTTCCGGTGC CATACTGAGCT  | 620 |

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 620 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

|  |     |
|--|-----|
| TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC  | 60  |
| TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA  | 120 |
| GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG  | 180 |
| TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGC   | 240 |
| CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCTTGGCG   | 300 |
| AACTCGTCGG CCAATTCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC   | 360 |
| GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG  | 420 |
| AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA  | 480 |
| GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC  | 540 |
| CATTCGTCTG GGGTGTTCGT CCATACGACC TCGATGCCGG TGGTGATCGC GTCCCTAACCG | 600 |
| GTTCCGGTGC CATACTGAGCT   | 620 |

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

|                       |    |
|-----------------------|----|
| AGAGTTTGAT CCTGGCTCAG | 20 |
|-----------------------|----|

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

|                    |    |
|--------------------|----|
| GGCGGACGGG TGAGTAA | 17 |
|--------------------|----|

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CTGCTGCCTC CCGTAGGAGT

20

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGACGTCAA GTCATCATGG CCCTTACGA

29

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTACAAGGCC CGGGAACGTA TTCACCG

27

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GCAACGAGCG CAACCC

16

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ATGACGTCAA GTCATCATGG CCCTTA

26

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

|  |      |
|--|------|
| AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA  | 60   |
| GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA  | 120  |
| TGTCCTGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT  | 180  |
| AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCAGATG  | 240  |
| GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGGCAC GATCCCTAGC TGGTCTGAGA  | 300  |
| GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG  | 360  |
| GGAATATTGC ACAATGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT   | 420  |
| TCGGGTTGTA AAGTACTTTC AGCGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT   | 480  |
| GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG  | 540  |
| GGTGCAAGCG TTAATCGGAA TTACTGGCG TAAAGCGCAC GCAGGCGGTT TGTAAAGTCA   | 600  |
| GATGTGAAAT CCCCGGGCTC AACCTGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC   | 660  |
| GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTG GAGGAATACC  | 720  |
| GGTGGCGAAG GCGGCCCT GGACGAAGAC TGACGCTCAG GTGCGAAAGC GTGGGGAGCA    | 780  |
| AACAGGATTA GATACTCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC  | 840  |
| CTTGAGGCCTT GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGAG TACGGCCGCA  | 900  |
| AGGTTAAAAC TCAAATGAAT TGACGGGGC CCGCACAAAGC GGTGGAGCAT GTGGTTAAAT  | 960  |
| TCGATGCAAC GCGAAGAAC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG   | 1020 |
| AATGTGCCCT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTGTGA   | 1080 |
| AATGTTGGGT TAAGTCCCGC AACGAGCGCA ACCCTTATCC TTTGTTGCCA GCGGTCCGGC  | 1140 |
| CGGAACTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG ACGTCAAGTC   | 1200 |
| ATCATGGCCC TTACGACCAAG GGCTACACAC GTGCTACAAT GGCGCATACA AAGAGAAGCG | 1260 |
| ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TGGCTCGTAG TCCGGATTGG AGTCTGCAAC  | 1320 |
| TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACG GTGAATACGT  | 1380 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| TCCCGGGCCT | TGTACACACC | GCCCCTCACA | CCATGGGAGT | GGGTTGCAAA | AGAAGTAGGT | 1440 |
| AGCTTAACCT | TCGGGAGGGC | GCTTACCACT | TTGTGATTCA | TGACTGGGT  | GAAGTCGTA  | 1500 |
| CAAGGTAACC | GTAGGGGAAC | CTGCGGTTGG | ATCACCTCCT | TA         |            | 1542 |

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1513 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

|            |            |             |             |            |            |      |
|------------|------------|-------------|-------------|------------|------------|------|
| TTTTTATGGA | GAGTTTGATC | CTGGCTCAGA  | GTGAACGCTG  | GCGGCGTGCC | TAATACATGC | 60   |
| AAGTCGAACG | ATGAAGCTTC | TAGCTTGCTA  | GAAGTGGATT  | AGTGGCGCAC | GGGTGAGTAA | 120  |
| GGTATAGTTA | ATCTGCCCTA | CACAAGAGGA  | CAACAGTTGG  | AAACGACTGC | TAATACTCTA | 180  |
| TACTCCTGCT | TAACACAAGT | TGAGTAGGGGA | AAGTTTTCTG  | GTGTAGGATG | AGACTATATA | 240  |
| GTATCAGCTA | GTTGGTAAGG | TAATGGCTTA  | CCAAGGCTAT  | GACGCTTAAC | TGGTCTGAGA | 300  |
| GGATGATCAG | TCACACTGGA | ACTGAGACAC  | GGTCCAGACT  | CCTACGGGAG | GCAGCAGTAG | 360  |
| GGAATATTGC | GCAATGGGGG | AAACCTGAC   | GCAGCAACGC  | CGCGTGGAGG | ATGACACTTT | 420  |
| TCGGAGCGTA | AACTCCTTTT | CTTAGGGAAG  | AATTCTGACG  | GTACCTAAGG | AATAAGCACC | 480  |
| GGCTAACTCC | GTGCCAGCAG | CCGCGGTAAT  | ACGGAGGGTG  | CAAGCGTTAC | TCGGAATCAC | 540  |
| TGGCGTAAA  | GGGCGCGTAG | GCGGATTATC  | AAGTCTCTTG  | TGAAATCTAA | TGGCTTAACC | 600  |
| ATTAAACTGC | TTGGGAAACT | GATAGTCTAG  | AGTGAGGGAG  | AGGCAGATGG | AATTGGTGGT | 660  |
| GTAGGGTAA  | AATCCGTAGA | TATCACCAAG  | AATAACCCATT | GCGAAGGCGA | TCTGCTGGAA | 720  |
| CTCAACTGAC | GCTAAGGCGC | GAAAGCGTGG  | GGAGCAAACA  | GGATTAGATA | CCCTGGTAGT | 780  |
| CCACGCCCTA | AACGATGTAC | ACTAGTTGTT  | GGGGTGCTAG  | TCATCTCAGT | AATGCAGCTA | 840  |
| ACGCATTAAG | TGTACCGCCT | GGGGAGTACG  | GTCGCAAGAT  | AAAAACTCAA | AGGAATAGAC | 900  |
| GGGGACCCGC | ACAAGCGGTG | GAGCATGTGG  | TTTAATTCGA  | AGATACGCGA | AGAACCTTAC | 960  |
| CTGGGCTTGA | TATCCTAAGA | ACCTTTAGA   | GATAAGAGGG  | TGCTAGCTTG | CTAGAACTTA | 1020 |
| GAGACAGGTG | CTGCACGGCT | GTCGTCAGCT  | CGTGTGCGTA  | GATGTTGGGT | TAAGTCCCGC | 1080 |
| AACGAGCGCA | ACCCACGTAT | TTAGTTGCTA  | ACGGTTCGGC  | CGAGCACTCT | AAATAGACTG | 1140 |
| CCTTCGTAAG | GAGGAGGAAG | GTGTGGACGA  | CGTCAAGTCA  | TCATGGCCCT | TATGCCAGG  | 1200 |
| GCGACACACG | TGCTACAATG | GCATATAGAA  | TGAGACGCAA  | TACCGCGAGG | TGGAGCAAAT | 1260 |
| CTATAAAATA | TGTCCCAGTT | CGGATTGTTTC | TCTGCAACTC  | GAGAGCATGA | AGCCGGAATC | 1320 |

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| GCTAGTAATC | GTAGATCAGC | CATGCTACGG | TGAATACGTT | CCCGGGTCTT | GTACTCACCG | 1380 |
| CCCGTCACAC | CATGGGAGTT | GATTCACTC  | GAAGCCGGAA | TACTAAACTA | GTTACCGTCC | 1440 |
| ACAGTGAAT  | CAGCGACTGG | GGTGAAGTCG | TAACAAGGTA | ACCGTAGGAG | AACCTGCGGT | 1500 |
| TGGATCACCT | CCT        |            |            |            |            | 1513 |

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1555 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

|             |            |             |            |             |             |      |
|-------------|------------|-------------|------------|-------------|-------------|------|
| TTTTATGGAG  | AGTTTGATCC | TGGCTCAGGA  | TGAACGCTGG | CGGCGTGCGCT | AATAACATGCA | 60   |
| AGTCGAGCGA  | ACGGACGAGA | AGCTTGCTTC  | TCTGATGTTA | GC GGCGGACG | GGTGAGTAAC  | 120  |
| ACGTGGATAA  | CCTACCTATA | AGACTGGGAT  | AACTTCGGGA | AACCGGAGCT  | AATAACGGAT  | 180  |
| AATATTTGA   | ACCGCATGGT | TCAAAAGTGA  | AAGACGGTCT | TGCTGTCACT  | TATAGATGGA  | 240  |
| TCCCGCCTGC  | ATTAGCTAGT | TGGTAAGGTA  | ACGGCTTACC | AAGGCAACGA  | TACGTAGCCG  | 300  |
| ACCTGAGAGG  | GTGATCGGCC | ACACTGGAAC  | TGAGACACGG | TCCAGACTCC  | TACGGGAGGC  | 360  |
| AGCAGTAGGG  | AATCTTCCGC | AATGGGCGAA  | AGCCTGACGG | AGCAACGCCG  | CGTGAGTGAT  | 420  |
| GAAGGTCTTC  | GGATCGTAAA | ACTCTGTTAT  | TAGGAAAGAA | CATATGTGTA  | AGTAACGTG   | 480  |
| CACATCTTGA  | CGGTACCTAA | TCAGAAAGCC  | ACGGCTAACT | ACGTGCCAGC  | AGCCGCGGTA  | 540  |
| ATACGTAGGT  | GGCAAGCGTT | ATCCGGAATT  | ATTGGGCGTA | AAGCGCGCGT  | AGGC GGTTTT | 600  |
| TTAAGTCTGA  | TGTGAAAGCC | CACGGCTCAA  | CCGTGGAGGG | TCATTGGAAA  | CTGGAAAAC   | 660  |
| TGAGTGCAGA  | AGAGGAAAGT | GGAATTCCAT  | GTGTAGCGGT | GAAATGCGCA  | GAGATATGGA  | 720  |
| GGAACACCAAG | TGGCGAAGGC | GACTTTCTGG  | TCTGTAACTG | ACGCTGATGT  | GCGAAAGCGT  | 780  |
| GGGGATCAAA  | CAGGATTAGA | TACCCCTGGTA | GTCCACGCCG | TAAACGATGA  | GTGCTAAGTG  | 840  |
| TTAGGGGGTT  | TCCGCCCTT  | AGTGCTGCAG  | CTAACGCATT | AAGCACTCCG  | CCTGGGGAGT  | 900  |
| ACGACCGCAA  | GGTTGAAACT | CAAAGGAATT  | GACGGGGACC | CGCACAAGCG  | GTGGAGCATG  | 960  |
| TGGTTTAATT  | CGAAGCAACG | CGAAGAACCT  | TACCAAATCT | TGACATCCTT  | TGACAACCTCT | 1020 |
| AGAGATAGAG  | CCTTCCCCTT | CGGGGGACAA  | AGTGACAGGT | GGTGCATGGT  | TGTCGTCAGC  | 1080 |
| TCGTGTCGTG  | AGATGTTGGG | TTAAGTCCCG  | CAACGAGCGC | AACCCCTTAAG | CTTAGTTGCC  | 1140 |
| ATCATTAAAGT | TGGGCACTCT | AAGTTGACTG  | CCGGTGACAA | ACCGGAGGAA  | GGTGGGGATG  | 1200 |
| ACGTCAAATC  | ATCATGCC   | TTATGATTTG  | GGCTACACAC | GTGCTACAAT  | GGACAATACA  | 1260 |

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| AAGGGCAGCG  | AAACCGCGAG | GTCAAGCAAA | TCCCATAAAG | TTGTTCTCAG | TTCGGATTGT | 1320 |
| AGTCTGCAAC  | TCGACTACAT | GAAGCTGGAA | TCGCTAGTAA | TCGTAGATCA | GCATGCTACG | 1380 |
| GTGAATACTGT | TCCCGGGTAT | TGTACACACC | GCCCCTCACA | CCACGAGAGT | TTGTAACACC | 1440 |
| CGAAGCCGGT  | GGAGTAACCT | TTTAGGAGCT | AGCCGTCGAA | GGTGGGACAA | ATGATTGGGG | 1500 |
| TGAAGTCGTA  | ACAAGGTAGC | CGTATCGGAA | GGTGCGGCTG | GATCACCTCC | TTTCT      | 1555 |